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Research Article

Morpho-phylogenetic evidence reveals five novel species of *Pestalotiopsis* (Sporocadaceae, Amphisphaeriales) from southern China

Ming-Gen Liao[1], Fang-Hua Guo[1], Xing-Xing Luo[1], Lian-Hu Zhang[1], Ru-Qiang Cui[1], Zhao-Huan Xu[1], Xiu-Guo Zhang[2], Jian Ma[1,3]

1 *College of Agronomy, Jiangxi Agricultural University, Nanchang, Jiangxi 330045, China*
2 *College of Plant Protection, Shandong Agricultural University, Taian, Shandong, 271018, China*
3 *Jiangxi Key Laboratory for Excavation and Utilization of Agricultural Microorganisms, Jiangxi Agricultural University, Nanchang, Jiangxi 330045, China*

Corresponding author: Jian Ma (majian821210@163.com)

Abstract

Pestalotioid fungi occurring as plant pathogens, endophytes, or saprophytes exhibit a wide range of plant hosts. During our ongoing mycological surveys in southern China, 21 strains of *Pestalotiopsis* were isolated from diseased leaves of terrestrial plants. Phylogenetic analyses of ITS, *tef*1-α, and *tub*2 sequence data were performed using maximum likelihood and Bayesian inference to reveal their taxonomic placement within *Pestalotiopsis*. Both molecular phylogenetic analyses and morphological comparisons supported them as five new species of *Pestalotiopsis*, namely *P. acericola*, *P. corchorifolii*, *P. fraseri*, *P. goeppertiæ*, and *P. koelreuteriæ*, and one known species, *P. machiliana*. This study supplements the species diversity of *Pestalotiopsis* associated with multiple hosts in southern China.

Key words: Ascomycota, molecular phylogeny, new species, Sordariomycetes, taxonomy

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Introduction

Fungi represent one of the most diverse groups of organisms globally, playing critical roles in areas such as culinary value, ecological regulation, nutrient cycling, and innovative applications in biotechnology, medicine, and ecological conservation (Niego et al. 2023). Projections derived from host-association models estimate global fungal diversity at 2.2 to 3.8 million species, whereas high-throughput sequencing approaches yield substantially higher estimates in the range of 11.7 to 13.2 million species (Hawksworth and Lücking 2017; Hyde 2022). However, only around 200,000 fungal species have been discovered and formally documented in Fungal Names (FN, https://nmdc.cn/fungalnames/).

The genus *Pestalotiopsis* Steyaert was segregated from *Pestalotia* De Not. by Steyaert (1949) to accommodate those taxa with 5-celled conidia based on conidial forms, and *Pestalotiopsis maculans* (Corda) Nag Raj (≡ *Sporocadus maculans* Corda) was designated as the type species (Nag Raj 1985; Maharachchikumbura et al. 2014; Wijayawardene et al. 2017). *Pestalotiopsis* species are easily characterized by fusiform or subcylindrical, 5-celled conidia with three

pigmented median cells and the presence of apical and basal appendages (Ariyawansa and Hyde 2018; Yin et al. 2024). Maharachchikumbura et al. (2014) further proposed two segregated anamorphic genera from *Pestalotiopsis*, namely *Neopestalotiopsis* Maharachch., K.D. Hyde & Crous and *Pseudopestalotiopsis* Maharachch., K.D. Hyde & Crous, based on combined datasets (ITS, *tef*1-α, and *tub*2) and the conidial pigmentation of the three median cells. As a result, *Neopestalotiopsis* differs from *Pestalotiopsis* and *Pseudopestalotiopsis* by its conidia with versicolorous median cells, and *Pseudopestalotiopsis* can be distinguished from *Pestalotiopsis* by sequence data and its conidia with dark-colored concolorous median cells. *Pestalotiopsis* is a species-rich group with varied habitats distributed in tropical and temperate regions (Bate-Smith and Metcalfe 1957; Luo et al. 2024). To date, about 457 epithets of *Pestalotiopsis* are recorded in Index Fungorum (Index Fungorum 2025). Members of the genus are common phytopathogens causing a variety of plant diseases, also occurring as endophytes and saprophytes isolated from leaf tissues, soil substrates, and rotted leaves, with some species further implicated in human and animal infections (Zhang et al. 2012a; Monden et al. 2013; Li et al. 2024; Luo et al. 2024; Yin et al. 2024). Previous research on *Pestalotiopsis* across a spectrum of environments has revealed a range of ecological functions. For example, functioning as saprophytes, some species accelerate material decomposition, whereas as endophytes, some species serve as sources of novel compounds with medicinal, agricultural, and industrial relevance (Xu et al. 2010, 2014).

Maharachchikumbura et al. (2014) revised the genus *Pestalotiopsis* based on combined ITS, *tef*1-α, and *tub*2 sequence data and morphological characteristics. These loci demonstrated strong phylogenetic resolution at the genus level and have been widely adopted in subsequent phylogenetic studies (Lin et al. 2023; Sun et al. 2023; Wang et al. 2025). In this study, samples of diseased leaves were collected from southern China. Accordingly, based on morphological observations and phylogenetic analyses (ITS, *tef*1-α, and *tub*2), 21 strains were assigned to *Pestalotiopsis*, including five novel species, namely *P. acericola*, *P. corchorifolii*, *P. fraseri*, *P. goeppertiæ*, and *P. koelreuteriæ*, and one known species, *P. machiliana* X.X. Luo & Jian Ma. Detailed illustrations and morphological descriptions of these taxa are provided below.

Materials and methods

Sample collection, fungal isolation, and morphological observation

Samples of diseased plant leaves were collected from botanical gardens and forest parks in southern China. The samples were placed in sealed bags with filter paper and transported to the laboratory. Fungi were isolated according to the tissue isolation method described by Gao et al. (2014). Leaf tissues were transferred onto potato dextrose agar (PDA; 200 g potato, 20 g glucose, 20 g agar, and 1000 mL water) plates and cultured at 25 °C under alternating light and dark conditions (8 h/16 h) for seven days, after which cultural characteristics, including color, shape, and size, were observed and recorded. The microscopic structures of isolated fungi were examined using an Olympus BX53 light microscope equipped with an Olympus DP27 digital camera (Olympus Optical Co., Ltd., Tokyo, Japan) to describe their morphological characteristics. All fun-

gal strains were stored in 10% sterilized glycerin at 4 °C for further studies. The studied specimens and cultures were deposited in the Herbarium of Jiangxi Agricultural University, Plant Pathology, Nanchang, China (**HJAUP**).

DNA extraction, PCR amplification, and sequencing

After fungal cultures were grown at 25 °C under a light–dark cycle (8 h/16 h) for 14 days, fresh mycelia were scraped with a sterile needle and transferred into 2 mL centrifuge tubes for grinding with liquid nitrogen. Genomic DNA was extracted using the Solarbio Fungal Genomic DNA Extraction Kit (Beijing Solarbio Science & Technology Co., Ltd., Beijing, China) according to the manufacturer's protocol. DNA was amplified in a 25 μL PCR system consisting of 12.5 μL of 2 × Power Taq PCR MasterMix, 9.5 μL of double-distilled water (ddH_2O), 1 μL of DNA template, and 1 μL each of forward and reverse primers, targeting three loci: ITS, *tef*1-α, and *tub*2. The primer pairs and PCR programs are listed in Table 1. PCR amplification products were stained with ethidium bromide and examined by electrophoresis in 1% agarose gels. Purification and sequencing of the PCR products were performed by Hunan Youkanglai Biotechnology Co., Ltd. The obtained sequences were submitted to the GenBank database (www.ncbi.nlm.nih.gov, accessed on 1 December 2025; Table 2).

Phylogenetic analyses

According to recent publications (Hsu et al. 2024; Li et al. 2024; Luo et al. 2024; Zhao et al. 2024; Cao et al. 2025; Jiang et al. 2025; Wang et al. 2025), sequences of *Pestalotiopsis* species obtained from GenBank were selected for phylogenetic analyses together with the 21 strains in this study (Table 2). *Nonappendiculata quercina* (CBS 116061 and CBS 270.82) was used as the outgroup. All sequences were aligned using MAFFT v.7.526 (Katoh et al. 2019, https://mafft.cbrc.jp/alignment/server/). A combined multilocus sequence dataset comprising ITS, *tef*1-α, and *tub*2 was assembled and manually optimized to improve alignment and sequence accuracy using PhyloSuite v.1.2.2 (Zhang et al. 2020). Phylogenetic trees were constructed based on the concatenated dataset using maximum likelihood (ML) and Bayesian inference (BI) in PhyloSuite v.1.2.2 (Zhang et al. 2020). The optimal partition model (edge-linked) was selected using the ModelFinder function (Kalyaanamoorthy et al. 2017), with the BIC criterion applied for IQ-TREE construction and the AICc criterion implemented for MrBayes analysis. Maximum likelihood phylogenies were constructed using IQ-TREE (Nguyen et al. 2015) under an edge-linked partition model, with nodal support assessed through 10,000

Table 1. Primers and PCR program used in this study.

Locus	Primers		PCR program
	Name	Sequence 5'–3'	
ITS	ITS5	GGAAGTAAAAGTCGTAACAAGG	95 °C: 3 min, (95 °C: 15 s, 54 °C: 15 s, 72 °C: 30 s) × 35 cycles, 72 °C: 5 min
	ITS4	TCCTCCGCTTATTGATATGC	
*tef*1-α	EF1-728F	CATCGAGAAGTTCGAGAAGG	95 °C: 3 min, (95 °C: 15 s, 56 °C: 15 s, 72 °C: 30 s) × 35 cycles, 72 °C: 5 min
	EF1-986R	TACTTGAAGGAACCCTTACC	
*tub*2	Bt2a	GGTAACCAAATCGGTGCTGCTTTC	95 °C: 3 min, (95 °C: 15 s, 54 °C: 15 s, 72 °C: 30 s) × 35 cycles, 72 °C: 5 min
	Bt2b	ACCCTCAGTGTAGTGACCCTTGGC	

Table 2. *Pestalotiopsis* species with their GenBank accession numbers used in the phylogenetic analyses of this study. New sequences are in bold.

Species	Strain number	Host/substrate	Locality	GenBank accession number			References
				ITS	*tef*1-*α*	*tub*2	
Pestalotiopsis abietis	CFCC 53011^{T}	*Abies fargesii*	China	MK397013	MK622277	MK622280	Gu et al. (2021)
P. abietis	CFCC 53012	*Abies fargesii*	China	MK397014	MK622278	MK622281	
P. adusta	ICMP 6088^{T}	Refrigerator door	Fiji	JX399006	JX399070	JX399037	Maharachchikumbura et al. (2012)
P. acericola	**HJAUP C1856.1^{T}**	***Acer buergerianum***	**China**	**PX613543**	**PX617762**	**PX625971**	**This study**
P. acericola	**HJAUP C1856.2**	***Acer buergerianum***	**China**	**PX613544**	**PX617763**	**PX625972**	
P. acericola	**HJAUP C1856.3**	***Acer buergerianum***	**China**	**PX613545**	**PX617764**	**PX625973**	
P. acericola	**HJAUP C1856.4**	***Acer buergerianum***	**China**	**PX613546**	**PX617765**	**PX625974**	
P. aggestorum	LC 6301^{T}	*Camellia sinensis*	China	KX895015	KX895234	KX895348	Liu et al. (2017)
P. aggestorum	LC 8186	*Camellia sinensis*	China	KY464140	KY464150	KY464160	
P. alloschemones	CGMCC 3.23480^{T}	*Alloschemone occidentalis*	China	OR247981	OR361456	OR381056	Razaghi et al. (2024)
P. alpinicola	HJAUP C1644.221^{T}	*Alpinia zerumbet*	China	PP962274	PP952249	PP952219	Luo et al. (2024)
P. alpinicola	HJAUP C1644.222	*Alpinia zerumbet*	China	PP962275	PP952248	PP952220	
P. americana	CBS 111576^{T}	*Leucospermum cunei* × *conocarpodendron*	USA	MH553961	MH554379	MH554620	Liu et al. (2019)
P. anacardiacearum	IFRDCC 2397^{T}	*Mangifera indica*	China	KC247154	KC247156	KC247155	Maharachchikumbura et al. (2013a)
P. anhuiensis	CFCC 54791^{T}	*Cyclobalanopsis glauca*	China	ON007028	ON005045	ON005056	Jiang et al. (2022a)
P. aporosæ-dioicæ	SAUCC224004^{T}	*Aporosa dioica*	China	OR733506	OR912988	OR912985	Yin et al. (2024)
P. aporosæ-dioicæ	SAUCC224005	*Aporosa dioica*	China	OR733505	OR912989	OR912986	
P. appendiculata	CGMCC 3.23550^{T}	*Rhododendron decorum*	China	OP082431	OP185509	OP185516	Gu et al. (2022)
P. arceuthobii	CBS 434.65^{T}	*Arceuthobium campylopodum*	USA	KM199341	KM199516	KM199427	Maharachchikumbura et al. (2014)
P. arengæ	CBS 331.92^{T}	*Arenga undulatifolia*	Singapore	KM199340	KM199515	KM199426	Maharachchikumbura et al. (2014)
P. australasiæ	CBS 114126^{T}	*Knightia* sp.	New Zealand	KM199297	KM199499	KM199409	Maharachchikumbura et al. (2014)
P. australasiæ	CBS 114141	*Protea* sp.	New South Wales	KM199298	KM199501	KM199410	
P. australis	CBS 111503	*Protea neriifolia* × *susannæ* cv. 'Pink Ice'	South Africa	KM199331	KM199557	KM199382	Maharachchikumbura et al. (2014)
P. australis	CBS 114193^{T}	*Grevillea* sp.	New South Wales	KM199332	KM199475	KM199383	
P. biappendiculata	CGMCC 3.23487^{T}	*Rhododendron* sp.	China	OR247984	OR361459	OR381059	Razaghi et al. (2024)
P. biappendiculata	LC4282	*Rhododendron* sp.	China	OR247990	OR361465	OR381065	
P. biappendiculata	LC4283	*Rhododendron* sp.	China	OR247991	OR361466	OR381066	
P. biciliata	CBS 124463^{T}	*Platanus* × *hispanica*	Slovakia	KM199308	KM199505	KM199399	Maharachchikumbura et al. (2014)
P. biciliata	CBS 236.38	*Pæonia* sp.	Italy	KM199309	KM199506	KM199401	
P. brachiata	LC 2988^{T}	*Camellia* sp.	China	KX894933	KX895150	KX895265	Liu et al. (2017)
P. brachiata	LC 8188	*Camellia* sp.	China	KY464142	KY464152	KY464162	
P. brachiata	LC 8189	*Camellia* sp.	China	KY464143	KY464153	KY464163	
P. brassicæ	CBS 170.26^{T}	*Brassica napus*	New Zealand	KM199379	KM199558	–	Maharachchikumbura et al. (2014)
P. buxicola	CFCC 57357^{T}	*Buxus bodinieri*	China	PP965518	PP957899	PP957901	Jiang et al. (2025)
P. buxicola	CFCC 57358	*Buxus bodinieri*	China	PP965519	PP957900	PP957902	
*P. camelliicol*a	HJAUP C1804.22^{1}T	*Camellia japonica*	China	PP962357	PP952236	PP952229	Luo et al. (2024)
P. camelliicola	HJAUP C1804.222	*Camellia japonica*	China	PP962358	PP952235	PP952230	
P. camelliæ	MFLUCC 12–0277^{T}	*Camellia japonica*	China	JX399010	JX399074	JX399041	Zhang et al. (2012a)
P. camelliæ–oleiferæ	CSUFTCC 08^{T}	*Camelliæ oleiferæ*	China	OK493593	OK507963	OK562368	Li et al. (2021)
P. camelliæ–oleiferæ	CSUFTCC 09	*Camelliæ oleiferæ*	China	OK493594	OK507964	OK562369	
P. cangshanensis	CGMCC 3.23544^{T}	*Rhododendron delavayi*	China	OP082426	OP185510	OP185517	Gu et al. (2022)
P. castanopsidis	CFCC 54430^{T}	*Castanopsis lamontii*	China	OK339732	OK358493	OK358508	Jiang et al. (2022a)
P. castanopsidis	CFCC 54305	*Castanopsis hystrix*	China	OK339733	OK358494	OK358509	
P. castanopsidis	CFCC 54384	*Castanopsis hystrix*	China	OK339734	OK358495	OK358510	
P. chamæropis	CBS 186.71^{T}	*Chamærops humilis*	Italy	KM199326	KM199473	KM199391	Maharachchikumbura et al. (2014)

Species	Strain number	Host/substrate	Locality	GenBank accession number			References
				ITS	*tef*1-α	*tub*2	
P. chamæropis	CFCC 55122	*Quercus aliena*	China	OM746229	OM840001	OM839902	Jiang et al. (2022b)
P. chamæropis	CFCC 55023	*Castanopsis fissa*	China	OM746233	OM840005	OM839906	
P. changjiangensis	CFCC 54314^{T}	*Castanopsis tonkinensis*	China	OK339739	OK358500	OK358515	Jiang et al. (2022a)
P. changjiangensis	CFCC 54433	*Castanopsis hainanensis*	China	OK339740	OK358501	OK358516	
P. changjiangensis	CFCC 52803	*Cyclobalanopsis austrocochinchinensis*	China	OK339741	OK358502	OK358517	
P. chaoyangensis	CFCC 55549^{T}	*Euonymus japonicus*	China	OQ344763	OQ410582	OQ410584	Lin et al. (2023)
P. chaoyangensis	CFCC 58805	*Euonymus japonicus*	China	OQ344764	OQ410583	OQ410585	
P. chiangmaiensis	MFLUCC 22–0127^{T}	*Phyllostachys edulis*	Thailand	OP497990	OP753374	OP752137	Sun et al. (2023)
P. chiaroscuro	BRIP 72970^{T}	*Sporobolus natalensis*	Australia	OK422510	OK423753	OK423752	Crous et al. (2022)
P. chinensis	MFLUCC 12–0273^{T}	NA	China	JX398995	–	–	Maharachchikumbura et al. (2012)
P. clavata	MFLUCC 12–0268^{T}	*Buxus* sp.	China	JX398990	JX399056	JX399025	Maharachchikumbura et al. (2012)
P. colombiensis	CBS 118553^{T}	*Eucalyptus urograndis*	Colombia	KM199307	KM199488	KM199421	Maharachchikumbura et al. (2014)
P. corchorifolii	**HJAUP C1891.1^{T}**	***Rubus corchorifolius***	**China**	**PX613547**	**PX617766**	**PX625975**	**This study**
P. corchorifolii	**HJAUP C1891.2**	***Rubus corchorifolius***	**China**	**PX613548**	**PX617767**	**PX625976**	
P. corchorifolii	**HJAUP C1891.3**	***Rubus corchorifolius***	**China**	**PX613549**	**PX617768**	**PX625977**	
P. corchorifolii	**HJAUP C1891.4**	***Rubus corchorifolius***	**China**	**PX613550**	**PX617769**	**PX625978**	
P. corchorifolii	**HJAUP C1891.5**	***Rubus corchorifolius***	**China**	**PX613551**	**PX617770**	**PX625979**	
P. cratoxyli	CGMCC 3.23512^{T}	*Cratoxylum cochinchinense*	China	OR248005	OR361480	OR381080	Razaghi et al. (2024)
P. cratoxyli	LC8772	*Cratoxylum cochinchinense*	China	OR248004	OR361479	OR381079	
P. cyclobalanopsidis	CFCC 54328^{T}	*Cyclobalanopsis glauca*	China	OK339735	OK358496	OK358511	Jiang et al. (2022a)
P. cyclobalanopsidis	CFCC 55891	*Cyclobalanopsis glauca*	China	OK339736	OK358497	OK358512	
P. cyclosora	HJAUP C1724.221^{T}	*Cyclosorus interruptus*	China	PP962279	PP952247	PP952221	Luo et al. (2024)
P. cyclosora	HJAUP C1724.222	*Cyclosorus interruptus*	China	PP962280	PP952246	PP952222	
P. cyclosora	HJAUP C1725.221	*Microlepia marginata*	China	PP962281	PP952245	PP952223	
P. cyclosora	HJAUP C1725.222	*Microlepia marginata*	China	PP962282	PP952244	PP952233	
P. cyclosora	HJAUP C1726.221	*Punica granatum*	China	PP962283	PP952243	PP952224	
P. cyclosora	HJAUP C1726.222	*Punica granatum*	China	PP962284	PP952242	PP952232	
P. daliensis	CGMCC 3.23548^{T}	*Rhododendron decorum*	China	OP082429	OP185511	OP185518	Gu et al. (2022)
P. dianellæ	CBS 143421^{T}	*Dianella* sp.	Australia	MG386051	–	MG386164	Crous et al. (2017)
P. digitalis	MFLU 14–0208^{T}	*Digitalis purpurea*	New Zealand	KP781879	–	KP781883	Liu et al. (2015)
P. dilucida	LC3232^{T}	*Camellia sinensis*	China	KX894961	KX895178	KX895293	Liu et al. (2017)
P. dilucida	LC8184	*Camellia sinensis*	China	KY464138	KY464148	KY464158	
P. diploclisiæ	CBS 115587^{T}	*Diploclisia glaucescens*	China	KM199320	KM199486	KM199419	Maharachchikumbura et al. (2014)
P. disseminata	CBS 143904	*Persea americana*	New Zealand	MH554152	MH554587	MH554825	Liu et al. (2019)
P. disseminata	MEAN 1165	*Pinus pinea*	Portugal	MT374687	MT374699	MT374712	Silva et al. (2020)
P. diversiseta	MFLUCC 12–0287^{T}	*Rhododendron* sp.	China	JX399009	JX399073	JX399040	Maharachchikumbura et al. (2012)
P. doitungensis	MFLUCC 14–0115	*Dendrobium* sp.	Thailand	MK993574	MK975832	MK975837	Ma et al. (2019)
P. dracænæ	HGUP 4037^{T}	*Dracæna fragrans*	China	–	MT598644	MT598645	Ariyawansa et al. (2015)
P. dracænicola	MFLUCC 18–0913^{T}	*Dracæna* sp.	Thailand	MN962731	MN962732	MN962733	Chaiwan et al. (2020)
P. dracænicola	MFLUCC 18–0914	*Dracæna* sp.	Thailand	MN962734	MN962735	MN962736	
P. dracontomelonis	MFLU 14–0207	*Dracontomelon dao*	Thailand	KP781877	KP781880	–	Liu et al. (2015)
P. eleuthero–cocci	HMJAU 60189^{T}	*Eleutherococcus brachypus*	China	OL996126	–	–	Tian et al. (2022)
P. eleuthero–cocci	HMJAU 60190	*Eleutherococcus brachypus*	China	OL996127	–	OL898722	
P. endophytica	MFLUCC 18–0932^{T}	*Magnolia garrettii*	Thailand	MW263946	MW417119	–	de Silva et al. (2021)
P. endophytica	MFLUCC 18–0946	*Magnolia garrettii*	Thailand	MW263947	MW729384	–	

Species	Strain number	Host/substrate	Locality	GenBank accession number			References
				ITS	*tef*1-α	*tub*2	
P. ericacearum	IFRDCC 2439^{T}	*Rhododendron delavayi*	China	KC537807	KC537814	KC537821	Zhang et al. (2013)
P. eriobotryæ	HJAUP C1742.221^{T}	*Eriobotrya japonica*	China	PP962289	PP952238	PP952227	Luo et al. (2024)
P. eriobotryæ	HJAUP C1742.222	*Eriobotrya japonica*	China	PP962291	PP952237	PP952228	
P. etonensis	BRIP 66615^{T}	*Sporobolus jacquemontii*	Australia	MK966339	MK977635	MK977634	Crous et al. (2020)
P. exudata	CGMCC 3.23488^{T}	*Aucuba japonica*	China	OR247985	OR361460	OR381060	Razaghi et al. (2024)
P. exudata	LC15850	*Aucuba japonica*	China	OR247986	OR361461	OR381061	
P. ficicrescens	HGUP 861^{T}	*Camellia japonica*	China	MZ477311	MZ868328	MZ868301	Hyde et al. (2023)
P. ficicrescens	CGMCC 3.23471	Oleaceae	China	OR247980	OR361455	OR381055	Razaghi et al. (2024)
P. foliicola	CFCC 54440^{T}	*Castanopsis faberi*	China	ON007029	ON005046	ON005057	Jiang et al. (2022a)
P. foliicola	CFCC 57359	*Castanopsis faberi*	China	ON007030	ON005047	ON005058	
P. foliicola	CFCC 57360	*Castanopsis faberi*	China	ON007031	ON005048	ON005059	
P. formosana	NTUCC 17–009^{T}	Poaceae sp.	China	MH809381	MH809389	MH809385	Ariyawansa and Hyde (2018)
P. formosana	NTUCC 17–010	Poaceae sp.	China	MH809382	MH809390	MH809386	
P. fraseri	**HJAUP C1693.1^{T}**	***Photinia × fraseri***	**China**	**PX613552**	**PX617771**	**PX625980**	**This study**
P. fraseri	**HJAUP C1693.2**	***Photinia × fraseri***	**China**	**PX613553**	**PX617772**	**PX625981**	
P. fraseri	**HJAUP C1693.3**	***Photinia × fraseri***	**China**	**PX613554**	**PX617773**	**PX625982**	
P. fraseri	**HJAUP C1693.4**	***Photinia × fraseri***	**China**	**PX613555**	**PX617774**	**PX625983**	
P. furcata	MFLUCC 12–0054^{T}	*Camellia sinensis*	Thailand	JQ683724	JQ683740	JQ683708	Maharachchikumbura et al. (2013b)
P. furcata	LC6691	*Camellia sinensis*	China	KX895030	KX895248	KX895363	Liu et al. (2017)
P. fusiformis	CGMCC 3.23495^{T}	*Rhododendron* sp.	China	OR247995	OR361470	OR381070	Razaghi et al. (2024)
P. fusiformis	LC15852	*Rhododendron* sp.	China	OR247996	OR361471	OR381071	
P. fusoidea	CGMCC 3.23545^{T}	*Rhododendron delavayi*	China	OP082427	OP185512	OP185519	Gu et al. (2022)
P. ganzhouensis	CGMCC 3.23489^{T}	*Cinnamomum camphora*	China	OR247987	OR361462	OR381062	Razaghi et al. (2024)
P. ganzhouensis	LC5089	*Cinnamomum camphora*	China	OR247998	OR361473	OR381073	
P. gardeniæ	HJAUP C1729.221^{T}	*Gardenia jasminoides*	China	PP962285	PP952241	PP952225	Luo et al. (2024)
P. gardeniæ	HJAUP C1729.222	*Gardenia jasminoides*	China	PP962286	PP952240	PP952226	
P. gardeniæ	HJAUP C1729.223	*Gardenia jasminoides*	China	PP962287	PP952239	PP952231	
P. gaultheriæ	IFRD 411–014^{T}	*Gaultheria forrestii*	China	KC537805	KC537812	KC537819	Zhang et al. (2013)
P. gibbosa	NOF 3175^{T}	*Gaultheria shallon*	Canada	LC311589	LC311591	LC311590	Watanabe et al. (2018)
P. goeppertiae	**HJAUP C1919.1^{T}**	***Goeppertia makoyana***	**China**	**PX613556**	**PX617775**	**PX625984**	**This study**
P. goeppertiae	**HJAUP C1919.2**	***Goeppertia makoyana***	**China**	**PX613557**	**PX617776**	**PX625985**	
P. goeppertiae	**HJAUP C1919.3**	***Goeppertia makoyana***	**China**	**PX613558**	**PX617777**	**PX625986**	
P. goeppertiae	**HJAUP C1919.4**	***Goeppertia makoyana***	**China**	**PX613559**	**PX617778**	**PX625987**	
P. grevilleæ	CBS 114127^{T}	*Grevillea* sp.	Australia	KM199300	KM199504	KM199407	Maharachchikumbura et al. (2014)
P. guangdongensis	ZHKUCC 22–0016^{T}	*Arenga pinnata*	China	ON180762	ON221520	ON221548	Xiong et al. (2022)
P. guangdongensis	ZHKUCC 22–0017	*Arenga pinnata*	China	ON180763	ON221521	ON221549	
P. guangdongensis	ZHKUCC 22–0018	*Arenga pinnata*	China	ON180764	ON221522	ON221550	
P. guangxiensis	CFCC 54308^{T}	*Quercus griffithii*	China	OK339737	OK358498	OK358513	Jiang et al. (2022a)
P. guangxiensis	CFCC 54300	*Quercus griffithii*	China	OK339738	OK358499	OK358514	
P. guiyangensis	CFCC 70626^{T}	*Eriobotrya japonica*	China	PP784740	PP842629	PP842617	Zhang et al. (2024)
P. guizhouensis	CFCC 54803	*Cyclobalanopsis glauca*	China	ON007035	ON005052	ON005063	Jiang et al. (2022a)
P. guizhouensis	CFCC 57364^{T}	*Cyclobalanopsis glauca*	China	ON007036	ON005053	ON005064	
P. hawaiiensis	CBS 114491^{T}	*Leucospermum* sp.	USA	KM199339	KM199514	KM199428	Maharachchikumbura et al. (2014)
P. hederæ	HJAUP C1638.221^{T}	*Hedera helix*	China	PP962270	PP952252	PP952234	Luo et al. (2024)
P. hederæ	HJAUP C1638.222	*Hedera helix*	China	PP962271	–	PP952216	
P. hispanica	CBS 115391^{T}	*Protea* sp.	Spain	MH553981	MH554399	MH554640	Liu et al. (2019)
P. hollandica	CBS 265.33^{T}	*Sciadopitys verticillata*	Netherlands	KM199328	KM199481	KM199388	Maharachchikumbura et al. (2014)
P. hollandica	MEAN 1091	*Pinus pinea*	Portugal	MT374678	MT374691	MT374703	Silva et al. (2020)
P. humicola	CBS 336.97^{T}	Soil	Papua New Guinea	KM199317	KM199484	KM199420	Maharachchikumbura et al. (2014)

Species	Strain number	Host/substrate	Locality	GenBank accession number			References
				ITS	*tef*1-α	*tub*2	
P. hunanensis	CSUFTCC15^{T}	*Camellia oleifera*	China	OK493599	OK507969	OK562374	Li et al. (2021)
P. hunanensis	CSUFTCC18	*Camellia oleifera*	China	OK493600	OK507970	OK562375	
P. hydei	MFLUCC 20–0135^{T}	*Litsea petiolata*	Thailand	MW266063	MW251113	MW251112	Huanaluek et al. (2021)
P. iberica	CAA 1004^{T}	*Pinus radiata*	Spain	MW732248	MW759038	MW759035	Monteiro et al. (2022)
P. iberica	CAA 1006	*Pinus radiata*	Spain	MW732249	MW759039	MW759036	
P. inflexa	MFLUCC 12–0270^{T}	Unidentified tree	China	JX399008	JX399072	JX399039	Maharachchikumbura et al. (2012)
P. intermedia	MFLUCC 12–0259^{T}	Unidentified tree	China	JX398993	JX399059	JX399028	Maharachchikumbura et al. (2012)
P. italiana	MFLU 14–0214^{T}	*Cupressus glabra*	Italy	KP781878	KP781881	KP781882	Liu et al. (2015)
P. jesteri	MFLUCC12–0279	*Fagræa bodenii*	China	JX399012	JX399076	JX399043	Maharachchikumbura et al. (2012)
P. jiangmenensis	CFCC 72595^{T}	*Pinus massoniana*	China	PV259810	PV275131	PV275205	Wang et al. (2025)
P. jiangmenensis	CFCC 72596	*Pinus massoniana*	China	PV259811	PV275132	PV275206	
P. jiangsuensis	CFCC 59538	*Pinus massoniana*	China	OR533577	OR539186	OR539191	Li et al. (2024)
P. jiangsuensis	CFCC 59539	*Pinus massoniana*	China	OR533578	OR539187	OR539192	
P. jiangsuensis	CFCC 59542	*Pinus massoniana*	China	OR533581	OR539190	OR539195	
P. jiangxiensis	LC4399^{T}	*Camellia* sp.	China	KX895009	KX895227	KX895341	Liu et al. (2017)
P. jinchanghensis	LC6636^{T}	*Camellia sinensis*	China	KX895028	KX895247	KX895361	Liu et al. (2017)
P. jinchanghensis	LC8190	*Camellia sinensis*	China	KY464144	KY464154	KY464164	
P. kaki	KNU–PT–1804^{T}	*Diospyros kaki*	Korea	LC552953	LC553555	LC552954	Das et al. (2020)
P. kandelicola	NCYUCC 19–0355^{T}	*Kandelia candel*	China	MT560723	MT563102	MT563100	Hyde et al. (2020)
P. kenyana	CBS 442.67^{T}	*Coffea* sp.	Kenya	KM199302	KM199502	KM199395	Maharachchikumbura et al. (2014)
P. kenyana	LC6633	*Camellia sinensis*	China	KX895027	KX895246	KX895360	
P. kenyana	CFCC 54962	*Quercus aliena*	China	OM746237	OM840009	OM839910	Jiang et al. (2022a)
P. kenyana	CFCC 54805	*Cyclobalanopsis glauca*	China	OM746253	OM840025	OM839926	
P. kenyana	CFCC 55088	*Castanopsis fissa*	China	OM746254	OM840026	OM839927	
P. knightiæ	CBS 111963	*Knightia* sp.	New Zealand	KM199311	KM199495	KM199406	Maharachchikumbura et al. (2014)
P. knightiæ	CBS 114138^{T}	*Knightia* sp.	New Zealand	KM199310	KM199497	KM199408	
P. koelreuteriae	**HJAUP C2757.1^{T}**	***Koelreuteria paniculata***	**China**	**PX613560**	**PX617779**	**PX625988**	**This study**
P. koelreuteriae	**HJAUP C2757.2**	***Koelreuteria paniculata***	**China**	**PX613561**	**PX617780**	**PX625989**	
P. krabiensis	MFLUCC 16–0260^{T}	*Pandanus* sp.	Thailand	MH388360	MH388395	MH412722	Tibpromma et al. (2018)
P. leucadendri	CBS 121417^{T}	*Leucadendron* sp.	South Africa	MH553987	MH554412	MH554654	Liu et al. (2019)
P. leucospermi	CBS 114489^{T}	*Leucospermum*	USA	MH553978	MH554396	MH554637	Liu et al. (2019)
P. licualicola	HGUP 4057^{T}	*Licuala grandis*	China	KC492509	KC481684	KC481683	Geng et al. (2013)
P. lijiangensis	CFCC 50738^{T}	*Castanopsis carlesii* var. *spinulosa*	China	KU860520	KU844185	KU844184	Zhou et al. (2018)
P. linearis	MFLUCC 12–0271^{T}	*Trachelospermum* sp.	China	JX398992	JX399058	JX399027	Maharachchikumbura et al. (2012)
P. linguæ	ZHKUCC 22–0159^{T}	*Pyrrosia lingua*	China	OP094104	OP186110	OP186108	Li et al. (2023)
P. linguæ	ZHKUCC 22–0160	*Pyrrosia lingua*	China	OP094103	OP186109	OP186107	
P. lithocarpi	CFCC 55100^{T}	*Lithocarpus chiungchungensis*	China	OK339742	OK358503	OK358518	Jiang et al. (2022a)
P. lithocarpi	CFCC 55893	*Lithocarpus chiungchungensis*	China	OK339743	OK358504	OK358519	
P. lobata	CGMCC 3.23467^{T}	*Lithocarpus glaber*	China	OR247976	OR361451	OR381051	Razaghi et al. (2024)
P. lobata	LC15843	*Lithocarpus glaber*	China	OR247977	OR361452	OR381052	
P. loeiana	MFLUCC 22–0123^{T}	Dead leaves	Thailand	OP497988	OP737881	OP713769	Sun et al. (2023)
P. longiappendiculata	LC3013	*Camellia sinensis*	China	KX894939	KX895156	KX895271	Liu et al. (2017)
P. lushanensis	LC4344^{T}	*Camellia* sp.	China	KX895005	KX895223	KX895337	Liu et al. (2017)
P. lushanensis	LC8182	*Camellia* sp.	China	KY464136	KY464146	KY464156	
P. lushanensis	LC8183	*Camellia* sp.	China	KY464137	KY464147	KY464157	
P. lushanensis	CFCC 54894	*Quercus serrata*	China	OM746282	OM840054	OM839955	Jiang et al. (2022b)

Species	Strain number	Host/substrate	Locality	GenBank accession number			References
				ITS	*tef*1-α	*tub*2	
P. macadamiæ	BRIP 63738b^{T}	*Macadamia integrifolia*	Australia	KX186588	KX186621	KX186680	Akinsanmi et al. (2017)
P. macadamiæ	BRIP 63739b	*Macadamia integrifolia*	Australia	KX186587	KX186620	KX186679	
P. macadamiæ	BRIP 637441a	*Macadamia integrifolia*	Australia	KX186586	KX186619	KX186678	
P. machili	CGMCC 3.23511^{T}	*Machilus* sp.	China	OR248003	OR361478	OR381078	Razaghi et al. (2024)
P. machiliana	HJAUP C1790.221^{T}	*Machilus pauhoi*	China	PP962355	PP952253	PP952214	Luo et al. (2024)
P. machiliana	HJAUP C1790.222	*Machilus pauhoi*	China	PP962356	PP952254	PP952215	
P. machiliana	HJAUP C1704.221	*Rhododendron simsii*	China	PP962276	PP952255	PP952211	
P. machiliana	HJAUP C1704.222	*Rhododendron simsii*	China	PP962277	PP952256	PP952212	
P. machiliana	HJAUP C1704.223	*Rhododendron simsii*	China	PP962278	PP952257	PP952213	
P. machiliana	**HJAUP C2801.1**	***Bambusa multiplex***	**China**	**PX613562**	**PX617781**	**PX625990**	**This study**
P. machiliana	**HJAUP C2801.2**	***Bambusa multiplex***	**China**	**PX613563**	**PX617782**	**PX625991**	
P. malayana	CBS 102220^{T}	*Macaranga triloba*	Malaysia	KM199306	KM199482	KM199411	Maharachchikumbura et al. (2014)
P. mangifericola	HJAUP C1639.221^{T}	*Mangifera indica*	China	PP962272	PP952251	PP952217	Luo et al. (2024)
P. mangifericola	HJAUP C1639.222	*Mangifera indica*	China	PP962273	PP952250	PP952218	
P. manyueyuanensis	NTUPPMCC 18-165^{T}	*Ophiocordyceps* sp.	China	OR125060	OR126313	OR126306	Hsu et al. (2024)
P. manyueyuanensis	NTUPPMCC 22-012	*Ophiocordyceps* sp.	China	OR125061	OR126314	OR126307	
P. massoniana	CFCC 72593^{T}	*Pinus massoniana*	China	PV259820	PV275141	PV275215	Wang et al. (2025)
P. massoniana	CFCC 72594	*Pinus massoniana*	China	PV259821	PV275142	PV275216	
P. menhaiensis	YN3A1^{T}	*Camellia sinensis*	China	KU252272	KU252401	KU252488	Wang et al. (2019)
P. monochæta	CBS 144.97^{T}	*Quercus robur*	Netherlands	KM199327	KM199479	KM199386	Maharachchikumbura et al. (2014)
P. monochæta	CBS 440.83	*Taxus baccata*	Netherlands	KM199329	KM199480	KM199387	
P. multiappendiculata	CGMCC 3.23514^{T}	NA	China	OR248008	OR361483	OR381083	Razaghi et al. (2024)
P. multicolor	CFCC59981^{T}	*Taxus chinensis*	China	OQ626676	OQ714341	OQ714336	Wang et al. (2024)
P. multicolor	CFCC59982	*Taxus chinensis*	China	OQ771896	OQ779483	OQ779488	
P. nanjingensis	CSUFTCC20	*Camellia oleifera*	China	OK493603	OK507973	OK562378	Li et al. (2021)
P. nanjingensis	CSUFTCC04	*Camellia oleifera*	China	OK493604	OK507974	OK562379	
P. nanningensis	CSUFTCC10^{T}	*Camellia oleifera*	China	OK493596	OK507966	OK562371	Li et al. (2021)
P. nanningensis	CSUFTCC11	*Camellia oleifera*	China	OK493597	OK507967	OK562372	
P. nannuoensis	SAUCC232203^{T}	Unknown host	China	OR733504	OR912991	OR863909	Yin et al. (2024)
P. nannuoensis	SAUCC232204	Unknown host	China	OR733503	OR912992	OR863910	
P. neglecta	TAP1100^{T}	*Quercus myrsinæfolia*	Japan	AB482220	LC311600	LC311599	Watanabe et al. (2018)
P. neolitseæ	NTUCC 17–011^{T}	*Neolitsea villosa*	China	MH809383	MH809391	MH809387	Ariyawansa and Hyde (2018)
P. neolitseæ	CFCC 54590	*Lithocarpus amygdalifolius*	China	OK339744	OK358505	OK358520	Jiang et al. (2022a)
P. ningboensis	CFCC 72585^{T}	*Pinus elliottii*	China	PV259822	PV275143	PV275217	Wang et al. (2025)
P. ningboensis	CFCC 72586	*Pinus elliottii*	China	PV259823	PV275144	PV275218	
P. novæ–hollandiæ	CBS 130973^{T}	*Banksia grandis*	Australia	KM199337	KM199511	KM199425	Maharachchikumbura et al. (2014)
P. oryzæ	CBS 111522	*Telopea* sp.	USA	KM199294	KM199493	KM199394	Maharachchikumbura et al. (2014)
P. oryzæ	CBS 171.26	NA	Italy	KM199304	KM199494	KM199397	
P. oryzæ	CBS 353.69^{T}	*Oryza sativa*	Denmark	KM199299	KM199496	KM199398	
P. pallidotheæ	MAFF 240993^{T}	*Pieris japonica*	Japan	AB482220	LC311585	LC311584	Watanabe et al. (2010)
P. pandanicola	MFLUCC 16–0255^{T}	*Pandanus* sp.	Thailand	MH388361	MH388396	MH412723	Tibpromma et al. (2018)
P. papuana	CBS 331.96^{T}	Coastal soil	Papua New Guinea	KM199321	KM199491	KM199413	Maharachchikumbura et al. (2014)
P. papuana	CBS 887.96	*Cocos nucifera*	Papua New Guinea	KM199318	KM199492	KM199415	
P. parva	CBS 265.37	*Delonix regia*	NA	KM199312	KM199508	KM199404	Maharachchikumbura et al. (2014)
P. parva	CBS 278.35^{T}	*Leucothoe fontanesiana*	NA	KM199313	KM199509	KM199405	
P. photinicola	GZCC 16–0028^{T}	*Photinia serrulata*	China	KY092404	KY047662	KY047663	Chen et al. (2017)
P. phyllostachydis	ZHKUCC 23–0873^{T}	NA	China	OR343210	OR367675	OR367676	Zhao et al. (2024)
P. pini	MEAN 1092^{T}	*Pinus pinea*	Portugal	MT374680	MT374693	MT374705	Silva et al. (2020)
P. pinicola	KUMCC 19–0183^{T}	*Pinus armandii*	China	MN412636	MN417509	MN417507	Tibpromma et al. (2019)

Species	Strain number	Host/substrate	Locality	GenBank accession number			References
				ITS	*tef*1-α	*tub*2	
P. piraubensis	COAD 2165^{T}	*Psidium guajava*	Brazil	MH627381	MH643774	MH643773	Jayawardena et al. (2022)
P. portugallica	CBS 393.48^{T}	NA	Portugal	KM199335	KM199510	KM199422	Maharachchikumbura et al. (2014)
P. portugallica	CBS 684.85	*Camellia japonica*	New Zealand	MH554065	MH554501	MH554741	Liu et al. (2019)
P. pruni	CGMCC 3.23507^{T}	*Prunus cerasoides*	China	OR248001	OR361476	OR381076	Razaghi et al. (2024)
P. pruni	LC15860	*Prunus cerasoides*	China	OR248002	OR361477	OR381077	
P. rhaphiolepis	SAUCC367701^{T}	*Rhaphiolepis indica*	China	OR733502	OR912994	OR863906	Yin et al. (2024)
P. rhaphiolepis	SAUCC367702	*Rhaphiolepis indica*	China	OR733501	OR912995	OR863907	
P. rhizophoræ	MFLUCC 17–0416^{T}	*Rhizophora mucronata*	Thailand	MK764283	MK764327	MK764349	Norphanphoun et al. (2019)
P. rhizophoræ	MFLUCC 17–0417	*Rhizophora mucronata*	Thailand	MK764284	MK764328	MK764350	
P. rhododendri	IFRDCC 2399^{T}	*Rhododendron sinogrande*	China	KC537804	KC537811	KC537818	Norphanphoun et al. (2019)
P. rhodomyrtus	CFCC 54733	*Quercus aliena*	China	OM746310	OM840082	OM839983	Jiang et al. (2022b)
P. rhodomyrtus	CFCC 55052	*Cyclobalanopsis augustinii*	China	OM746311	OM840083	OM839984	
P. rosarioides	CGMCC 3.23549^{T}	*Rhododendron decorum*	China	OP082430	OP185513	OP185520	Gu et al. (2022)
P. rosea	MFLUCC 12–0258^{T}	*Pinus* sp.	China	JX399005	JX399069	JX399036	Maharachchikumbura et al. (2012)
P. rubræ	CGMCC 3.23499^{T}	*Quercus rubra*	China	OR247997	OR361472	OR381072	Razaghi et al. (2024)
P. rubræ	LC8233	*Plagiogyria glauca*	China	OR248000	OR361475	OR381075	
P. sabal	ZHKUCC 22–0027	*Sabal mexicana*	China	ON180765	ON221523	ON221551	Xiong et al. (2022)
P. sabal	ZHKUCC 22–0029	*Sabal mexicana*	China	ON180767	ON221525	ON221553	
P. schisandræ	CFCC 59550^{T}	*Schisandra sphenanthera*	China	OR775411	OR766002	OR766014	Yuan et al. (2024)
P. schisandræ	CFCC 59551	*Schisandra sphenanthera*	China	OR775412	OR766003	OR766015	
P. scoparia	CBS 176.25^{T}	*Chamæcyparis* sp.	China	KM199330	KM199478	KM199393	Maharachchikumbura et al. (2012)
P. sequoiæ	MFLUCC 13–0399^{T}	*Sequoia sempervirens*	Italy	KX572339	–	–	Maharachchikumbura et al. (2012)
P. shaanxiensis	CFCC 54958^{T}	*Quercus variabilis*	China	ON007026	ON005043	ON005054	Jiang et al. (2022a)
P. shaanxiensis	CFCC 57356	*Quercus variabilis*	China	ON007027	ON005044	ON005055	
P. shanweiensis	CFCC 72591^{T}	*Pinus massoniana*	China	PV259824	PV275145	PV275219	Wang et al. (2025)
P. shanweiensis	CFCC 72592	*Pinus massoniana*	China	PV259825	PV275146	PV275220	
P. shorea	MFLUCC 12–0314^{T}	*Shorea obtusa*	Thailand	KJ503811	KJ503817	KJ503814	Song et al. (2014)
P. sichuanensis	SC3A21^{T}	*Camellia sinensis*	China	KX146689	KX146748	KX146807	Wang et al. (2019)
P. silvicola	CFCC 55296^{T}	*Cyclobalanopsis kerrii*	China	ON007032	ON005049	ON005060	Jiang et al. (2022a)
P. silvicola	CFCC 54915	*Cyclobalanopsis kerrii*	China	ON007033	ON005050	ON005061	
P. silvicola	CFCC 57363	*Cyclobalanopsis kerrii*	China	ON007034	ON005051	ON005062	
P. smilacicola	MFLUCC 22–0125^{T}	*Smilax* sp.	Thailand	OP497991	OP753376	OP762673	Sun et al. (2023)
P. solicola	SAUCC003804^{T}	Soil	China	OQ692020	OQ718737	OQ718795	Li et al. (2024)
P. solicola	SAUCC003806	Soil	China	OQ692021	OQ718738	OQ718796	
P. solicola	SAUCC003807	Soil	China	OQ692022	OQ718739	OQ718797	
P. sonneratiæ	CFCC 57392	*Sonneratia apetala*	China	ON114182	ON086810	ON086814	Jiang et al. (2022c)
P. sonneratiæ	CFCC 57394^{T}	*Sonneratia apetala*	China	ON114184	ON086812	ON086816	
P. sonneratiæ	CFCC 57395	*Sonneratia apetala*	China	ON114185	ON086813	ON086817	
P. spathulata	CBS 356.86^{T}	*Gevuina avellana*	Chile	KM199338	KM199513	KM199423	Maharachchikumbura et al. (2014)
P. spathuliappendiculata	CBS 144035^{T}	*Phoenix canariensis*	Australia	MH554172	MH554607	MH554845	Liu et al. (2019)
P. suæ	CGMCC 3.23546^{T}	*Rhododendron delavayi*	China	OP082428	OP185514	OP185521	Gu et al. (2022)
P. taxicola	CFCC59976^{T}	*Taxus chinensis*	China	OQ626673	OQ714338	OQ714333	Wang et al. (2024)
P. taxicola	CFCC59978	*Taxus chinensis*	China	OQ771893	OQ779480	OQ779485	
P. telopeæ	CBS 114137	*Protea* sp.	Australia	KM199301	KM199559	KM199469	Maharachchikumbura et al. (2014)
P. telopeæ	CBS 114161^{T}	*Telopea* sp.	Australia	KM199296	KM199500	KM199403	
P. telopeæ	CBS 113606	*Telopea* sp.	Australia	KM199295	KM199498	KM199402	
P. terricola	CBS 141.69^{T}	Soil	Pacific Islands	MH554004	MH554438	MH554680	Liu et al. (2019)

Species	Strain number	Host/substrate	Locality	GenBank accession number			References
				ITS	*tef*1-α	*tub*2	
P. thailandica	MFLUCC 17–1616^{T}	*Rhizophora apiculata*	Thailand	MK764286	MK764330	MK764352	Maharachchikumbura et al. (2014)
P. thailandica	MFLUCC 17–1617	*Rhizophora apiculata*	Thailand	MK764285	MK764329	MK764351	
P. thunbergii	CFCC 72589^{T}	*Pinus thunbergii*	China	PV259838	PV275159	PV275233	Wang et al. (2025)
P. thunbergii	CFCC 72590	*Pinus thunbergii*	China	PV259839	PV275160	PV275234	
*P. trachycarpico*la	OP068^{T}	*Trachycarpus fortunei*	China	JQ845947	JQ845946	JQ845945	Zhang et al. (2012b)
P. trachycarpicola	OP143	*Podocarpus macrophyllus*	China	KC537809	KC537816	KC537823	
P. trachycarpicola	MFLUCC 12-0267	Unidentified tree	China	JX399001	JX399065	JX399032	Maharachchikumbura et al. (2012)
P. tumida	CFCC 55158^{T}	*Rosa chinensis*	China	OK560610	OL814524	OM158174	Peng et al. (2022)
P. tumida	CFCC 55159	*Rosa chinensis*	China	OK560613	OL814527	OM158177	
P. unicolor	MFLUCC 12–0276^{T}	*Rhododendron* sp.	China	JX398999	–	JX399030	Maharachchikumbura et al. (2012)
P. verruculosa	MFLUCC 12–0274^{T}	*Rhododendron* sp.	China	JX398996	JX399061	–	Maharachchikumbura et al. (2012)
P. wenzhouensis	CFCC 72587^{T}	*Pinus massoniana*	China	PV259840	PV275161	PV275235	Wang et al. (2025)
P. wenzhouensis	CFCC 72588	*Pinus massoniana*	China	PV259845	PV275166	PV275240	
P. wulichongensis	CGMCC 3.23469^{T}	Poaceae	China	OR247978	OR361453	OR381053	Razaghi et al. (2024)
P. wulichongensis	LC15846	Poaceae	China	OR247979	OR361454	OR381054	
P. yanglingensis	LC 4553^{T}	*Camellia sinensis*	China	KX895012	KX895231	KX895345	Liu et al. (2017)
P. yunnanensis	HMAS 96359^{T}	*Podocarpus macrophyllus*	China	AY373375	–	–	Wei et al. (2013)
Nonappendiculata quercina	CBS 116061^{T}	*Quercus suber*	Italy	MH553982	MH554400	MH554641	Liu et al. (2019)
N. quercina	CBS 270.82	*Quercus pubescens*	Italy	MH554025	MH554459	MH554701	

The ex-type strains are indicated using "^{T}" after strain numbers; "–" stands for no sequence data in GenBank.

ultrafast bootstrap replicates (Minh et al. 2013). The final phylogenetic tree was selected from suboptimal trees of each run through likelihood score comparison, with the following models applied to respective gene partitions: HKY+F+R5 for ITS, TIM2e+R4 for *tef*1-α, and TPM2u+F+I+G4 for *tub*2. Bayesian inference phylogenies were constructed using MrBayes v.3.2.6 (Ronquist et al. 2012) under a partition model configuration, with two parallel runs and 2,000,000 generations, while discarding the initial 25% of sampled data as burn-in. The best-fit models were HKY+F+I+G4 for ITS, GTR+F+G4 for *tef*1-α, and GTR+F+I+G4 for *tub*2. Phylogenetic trees were visualized using FigTree v.1.4.4 (http://tree.bio.ed.ac.uk/software/figtree), with subsequent editing and layout finalized in Adobe Illustrator CS v.5.

Results

Molecular phylogeny

Based on the concatenated sequences of the three barcode genes (ITS, *tef*1-α, and *tub*2), the phylogenetic tree (Fig. 1) was constructed using maximum likelihood (ML) and Bayesian inference (BI) to analyze the phylogenetic relationships of the 21 strains within the genus *Pestalotiopsis*. The phylogenetic analyses included 301 strains (Table 1), comprising 159 accepted *Pestalotiopsis* species and 21 strains from this study, with *Nonappendiculata quercina* (CBS 116061 and CBS 270.82) serving as the outgroup. The combined sequence consisted of 1472 nucleotide positions (ITS: 1–556, *tef*1-α: 557–1013, *tub*2: 1014–1472), comprising 901 distinct patterns, 662 parsimony-informative sites, 163 singleton sites, and 647 constant sites. Phylogenetic trees were constructed based on the concatenated sequences using ML and BI methods with essentially identical topological

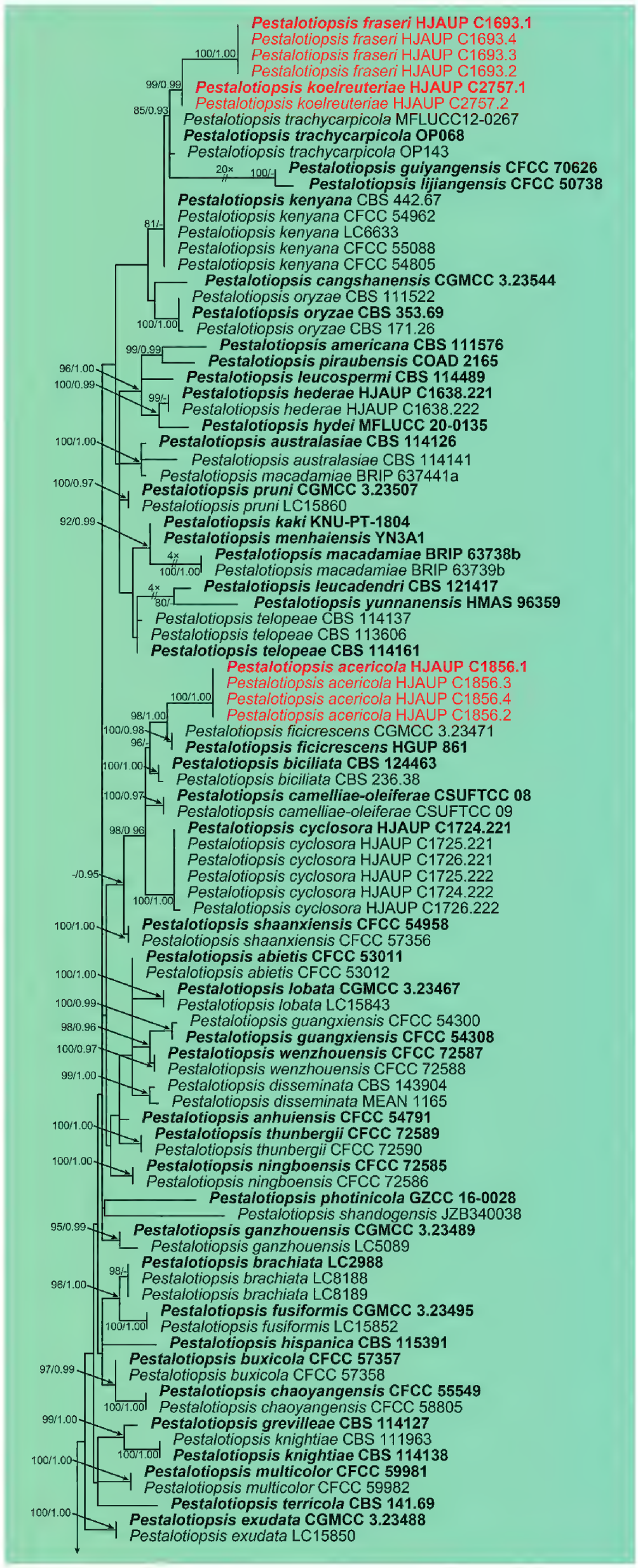

Figure 1. A maximum-likelihood phylogenetic tree of *Pestalotiopsis* constructed based on concatenated sequence data of ITS, *tef*1-α, and *tub*2. Bootstrap support values for ML greater than 80% and Bayesian posterior probabilities greater than 0.95 are shown near the nodes. The tree is rooted with *Nonappendiculata quercina* (CBS 116061 and CBS 270.82). New strains identified in this study are shown in blue; new species are shown in red. Some branches were shortened according to the indicated multipliers, and these are indicated by the symbol (//).

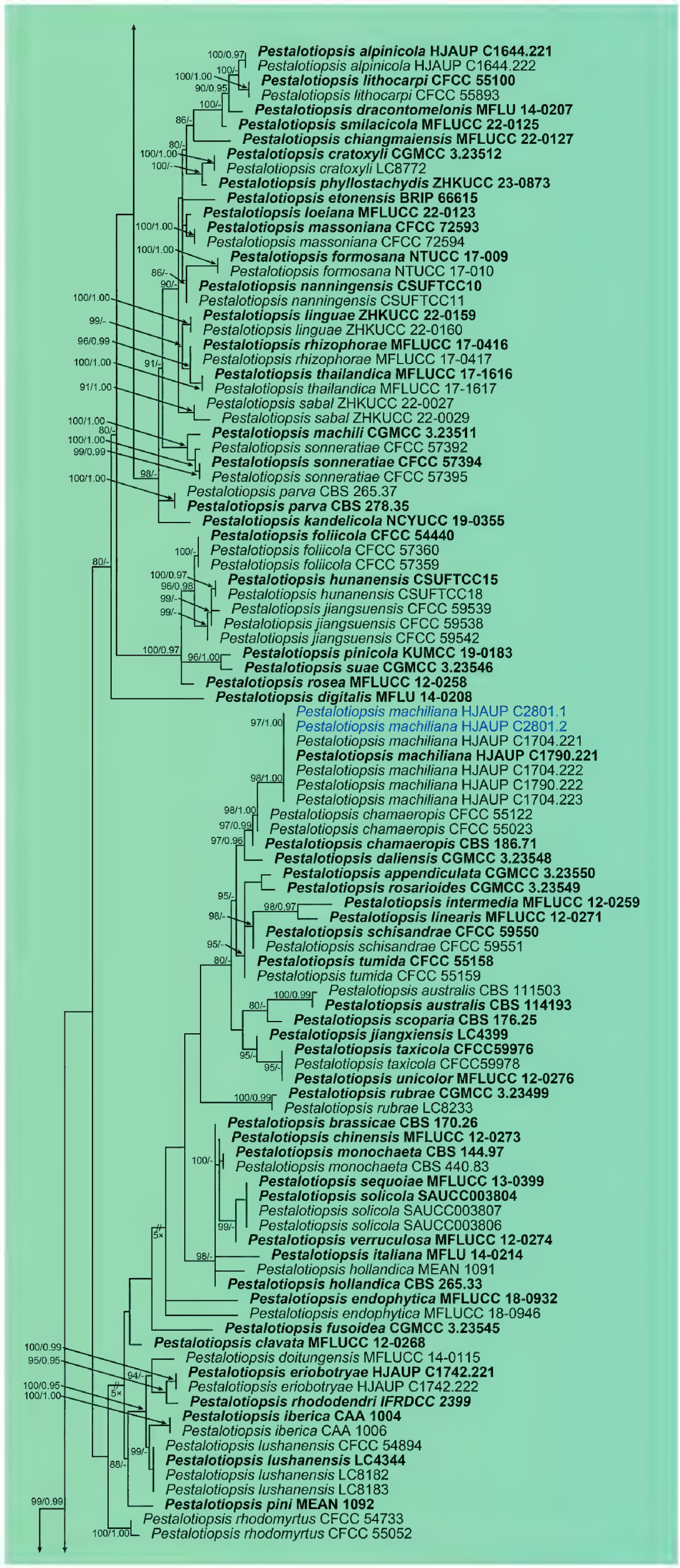

Figure 1. Continued.

Figure 1. Continued.

architectures. The optimal ML phylogenetic tree (lnL = −19450.797) is shown in Fig. 1, with node support values annotated adjacent to each branch. At each node, the first and second numerical descriptors correspond to ultrafast bootstrap support values from ML and posterior probabilities obtained from BI, respectively.

Taxonomy

Pestalotiopsis acericola **M.G. Liao & Jian Ma, sp. nov.**
Index Fungorum: IF904707
Fig. 2

Type. CHINA • Zhejiang Province, Hangzhou City, West Lake Scenic Area, on diseased leaves of *Acer buergerianum*, 22 October 2023, X.X. Luo (HJAUP M1856, ***holotype***), ex-type living culture, HJAUP C1856.1 = HJAUP C1856.2 = HJAUP C1856.3 = HJAUP C1856.4.

Etymology. Named after the genus, *Acer*, from which the fungus was isolated.

Description. Regular leaf spots, grey white in center with blurred margin. **Asexual morph on PDA:** Conidiomata acervular, globose to clavate, 350–660 µm diam., superficial, solitary or aggregated in clusters, black. Conidiophores indistinct and reduced to conidiogenous cells. Conidiogenous cells hyaline, smooth, cylindrical to ampulliform. Conidia fusiform, straight or slightly curved, 16.1–24.5 × 5.2–6.9 µm ($\bar{x}$ = 20.9 × 5.9 µm, n = 50), 4-septate, slightly constricted at the septa; basal cell conical, 3.1–5.3 µm ($\bar{x}$ = 4.1 µm), hyaline or sometimes pale brown, smooth, thin-walled, with a single filiform appendage, unbranched, 4.6–10.7 µm ($\bar{x}$ = 7.0 µm) long; three median cells doliiform to cylindrical, smooth, thick-walled, 10.4–14.6 µm ($\bar{x}$ = 12.8 µm), concolorous, pale brown to brown, somewhat constricted at the septa, second cell from the base 3.6–5.0 µm ($\bar{x}$ = 4.4 µm) long, third cell 3.0–5.0 µm ($\bar{x}$ = 4.1 µm) long, fourth cell 3.6–5.8 µm ($\bar{x}$ = 4.6 µm) long); apical cell conical to acute, hyaline, smooth, thin-walled, 2.6–4.6 µm ($\bar{x}$ = 3.9 µm) long, with 2–3 filiform appendages, arising from the apex of the apical cell each at a different point, unbranched, 12.3–27.5 µm ($\bar{x}$ = 17.7 µm) long. **Sexual morph:** not observed.

Culture characteristics. Colonies on PDA grow fast, filamentous, reaching 76–82 mm diam. after 5–7 days at 25 °C in light and dark conditions (8 h/16 h), white, with flocculent mycelium and entire edge, forming black, brown conidiomata, and reverse pale orange in center.

Note. Phylogenetic analyses revealed that the four strains (HJAUP C1856.1^{T}, HJAUP C1856.2, HJAUP C1856.3, and HJAUP C1856.4) of *P. acericola* form a distinct clade sister to *P. ficicrescens* (HGUP 861^{T} and CGMCC 3.23471) with 98% ML/1.00 BI bootstrap support (Fig. 1). Based on a BLASTn search of *P. acericola* (HJAUP C1856.1^{T}) and *P. ficicrescens* (HGUP 861^{T}) in GenBank, comparisons of nucleotides showed 2 bp (537/539, including two gaps), 1 bp (291/292, no gaps), and 4 bp (451/455, including one gap) nucleotide differences in the ITS, *tef*1-α, and *tub*2 regions, respectively. Moreover, *P. acericola* differs from *P. ficicrescens* Qi Yang & Yong Wang bis (Hyde et al. 2023) in its smaller conidiomata (350–660 µm diam. vs. 400–1200 µm diam.) and wider conidia (5.2–6.9 µm vs. 3–5.5 µm) with a longer fourth cell (3.6–5.8 µm vs. 3–5 µm) from the base, a longer basal appendage (4.6–10.7 µm vs. 3.5–7 µm), and longer apical appendages (12.3–27.5 µm vs. 10.5–18 µm). Furthermore, *P. acericola* can be distinguished from *P. ficicrescens* by its different host (*Acer buergerianum* vs. *Ficus tikoua*).

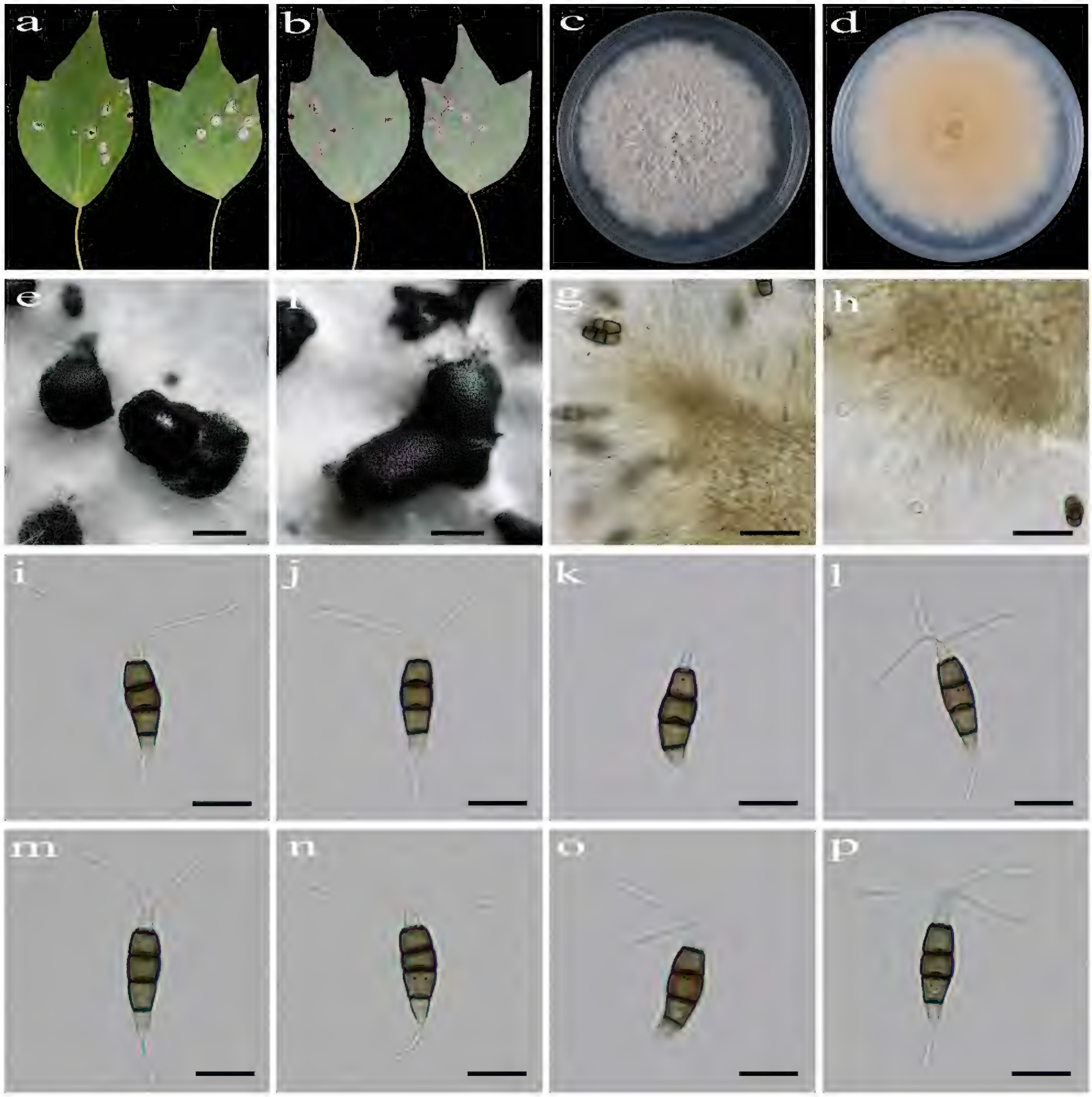

Figure 2. *Pestalotiopsis acericola* (HJAUP C1856.1, ex-type). **a, b.** Leaf of host plant (front and reverse); **c, d.** Culture on PDA (front and reverse); **e, f.** Conidiomata; **g, h.** Conidiogenous cells and conidia; **i–p.** Conidia. Scale bars: 400 μm (**e, f**); 20 μm (**g, h**); 10 μm (**i–p**).

Pestalotiopsis corchorifolii **M.G. Liao & Jian Ma, sp. nov.**

MycoBank No: 861554

Fig. 3

Type. CHINA • Zhejiang Province, Wenzhou City, Wenzhou Botanical Garden, on diseased leaves of *Rubus corchorifolius*, 24 October 2023, X.X. Luo (HJAUP M1891, ***holotype***), ex-type living culture HJAUP C1891.1 = HJAUP C1891.2 = HJAUP C1891.3 = HJAUP C1891.4 = HJAUP M1891.5.

Etymology. Named after the host species, *Rubus corchorifolius*, from which the fungus was isolated.

Description. Regular leaf spots, grey white in center with brown at margin. **Asexual morph on PDA:** Conidiomata acervular, globose to clavate, 849–1375 µm diam., solitary or aggregated in clusters, black. Conidiophores indistinct and reduced to conidiogenous cells. Conidiogenous cells hyaline, smooth, cylindrical to ampulliform. Conidia fusiform, straight or slightly curved, 14.6–21.6 × 4.4–5.9 µm ($\overline{x}$ = 17.4 × 5.3 µm, n = 50), 4-septate, slightly constricted at the septa; basal cell conical, 2.2–3.9 µm ($\overline{x}$ = 2.6 µm), hyaline, smooth, thin-walled, with a single filiform appendage, unbranched, 0.9–3.1 µm ($\overline{x}$ = 2.1 µm) long; three median cells doliiform to cylindrical, smooth, thick-walled, 10.5–14.0 µm ($\overline{x}$ = 12.1 µm), concolorous, brown, somewhat constricted at the septa, second cell from the base 3.4–5.6 µm ($\overline{x}$ = 4.1 µm) long, third cell 3.3–4.6 µm ($\overline{x}$ = 4.1

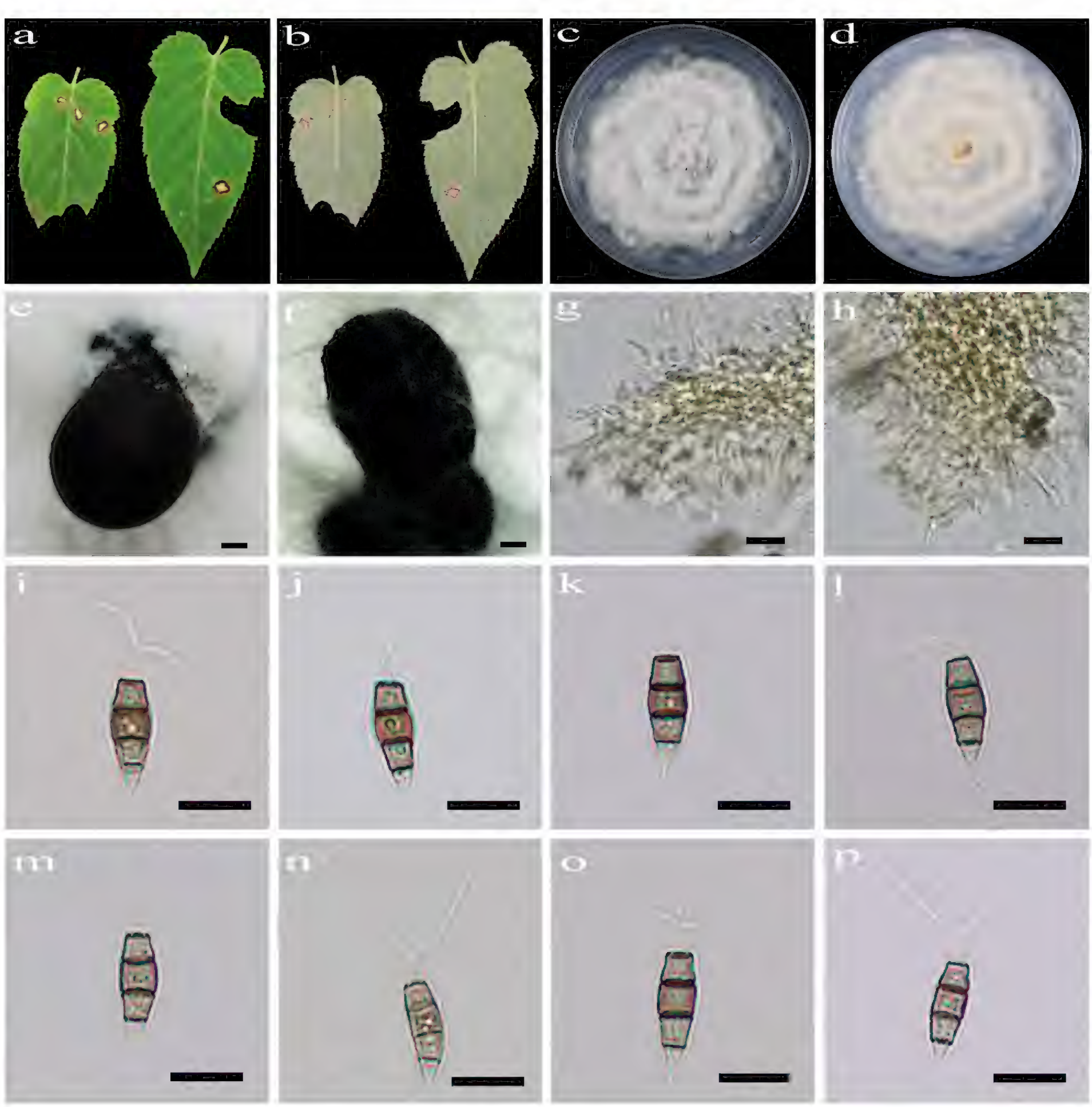

Figure 3. *Pestalotiopsis corchorifolii* (HJAUP C1891.1, ex-type). **a, b.** Leaf of host plant (front and reverse); **c, d.** Culture on PDA (front and reverse); **e, f.** Conidiomata; **g, h.** Conidiogenous cells and conidia; **i–p.** Conidia. Scale bars: 200 µm (**e, f**); 10 µm (**g–p**).

μm) long, fourth cell 3.4–4.7 μm ($\bar{x}$ = 4.0 μm) long); apical cell conical to acute, hyaline, smooth, thin-walled, 1.9–3.7 μm ($\bar{x}$ = 2.7 μm) long, with 2–3 filiform appendages, arising from the apex of the apical cell each at a different point, unbranched, 6.7–17.4 μm ($\bar{x}$ = 11.5 μm) long. **Sexual morph:** not observed.

Culture characteristics. Colonies on PDA grow fast, filamentous, reaching 85–90 mm diam. after 5–7 days at 25 °C in light and dark conditions (8 h/16 h), white, with flocculent mycelium and entire edge, forming black conidiomata, and reverse white.

Note. Phylogenetic analyses revealed that the five strains (HJAUP C1891.1^{T}, HJAUP C1891.2, HJAUP C1891.3, HJAUP C1891.4, and HJAUP M1891.5) of *P. corchorifolii* form a distinct clade sister to *P. camelliicola* (HJAUP C1804.221^{T} and HJAUP C1804.222) with 98% ML/1.00 BI bootstrap support (Fig. 1). Based on a BLASTn search of *P. corchorifolii* (HJAUP C1891.1^{T}) and *P. camelliicola* (HJAUP C1804.221^{T}) in GenBank, comparisons of nucleotides showed 1 bp (630/631, including one gap), 5 bp (296/301, including three gaps), and 5 bp (476/481, including one gap) nucleotide differences in the ITS, *tef*1-α, and *tub*2 regions, respectively. Moreover, *P. corchorifolii* can be distinguished from *P. camelliicola* X.X. Luo & Jian Ma (Luo et al. 2024) by its larger conidiomata (849–1375 μm diam. vs. 470–1320 μm diam.) and smooth, narrower conidia (4.4–5.9 μm vs. 5.7–7.6 μm), and further differs in that the conidia of *P. camelliicola* have 2–4 tubular apical appendages arising from an apical crest or irregularly branched along their length, resulting in 2–3 branches. Furthermore, *P. corchorifolii* can be distinguished from *P. camelliicola* by its different host (*Rubus corchorifolius* vs. *Camellia japonica*).

Pestalotiopsis fraseri **M.G. Liao & Jian Ma, sp. nov.**

MycoBank No: 861555

Fig. 4

Type. CHINA • Jiangxi Province, Nanchang City, Jiangxi Agricultural University, on diseased leaves of *Photinia* × *fraseri* Dress, 26 October 2023, X.X. Luo (HJAUP M1693, ***holotype***), ex-type living culture HJAUP C1693.1 = HJAUP C1693.2 = HJAUP C1693.3 = HJAUP C1693.4.

Etymology. Named after the host species, *Photinia* × *fraseri*, from which the fungus was isolated.

Description. Regular leaf spots, pale brown in center with brown at margin. **Asexual morph on PDA:** Conidiomata acervular, globose to clavate, 426–786 μm diam., solitary, black. Conidiophores indistinct and reduced to conidiogenous cells. Conidiogenous cells hyaline, smooth, cylindrical to ampulliform. Conidia fusiform, straight or slightly curved, 19.3–26.4 × 5.2–6.3 μm ($\bar{x}$ = 23.0 × 5.7 μm, n = 50), 4-septate, slightly constricted at the septa; basal cell conical, 3.4–5.3 μm ($\bar{x}$ = 4.4 μm), hyaline, smooth, thin-walled, with a single filiform appendage, unbranched, 4.6–10.5 μm ($\bar{x}$ = 7.9 μm) long; three median cells doliiform to cylindrical, smooth, thick-walled, 12.2–16.2 μm ($\bar{x}$ = 14.4 μm), concolorous, brown, somewhat constricted at the septa, second cell from the base 3.9–6.1 μm ($\bar{x}$ = 4.8 μm) long, third cell 4.0–5.4 μm ($\bar{x}$ = 4.7 μm) long, fourth cell 4.0–5.2 μm ($\bar{x}$ = 4.7 μm) long); apical cell conical to acute, hyaline, smooth, thin-walled, 3.7–5.0 μm ($\bar{x}$ = 4.2 μm) long, with 2–3 filiform appendag-

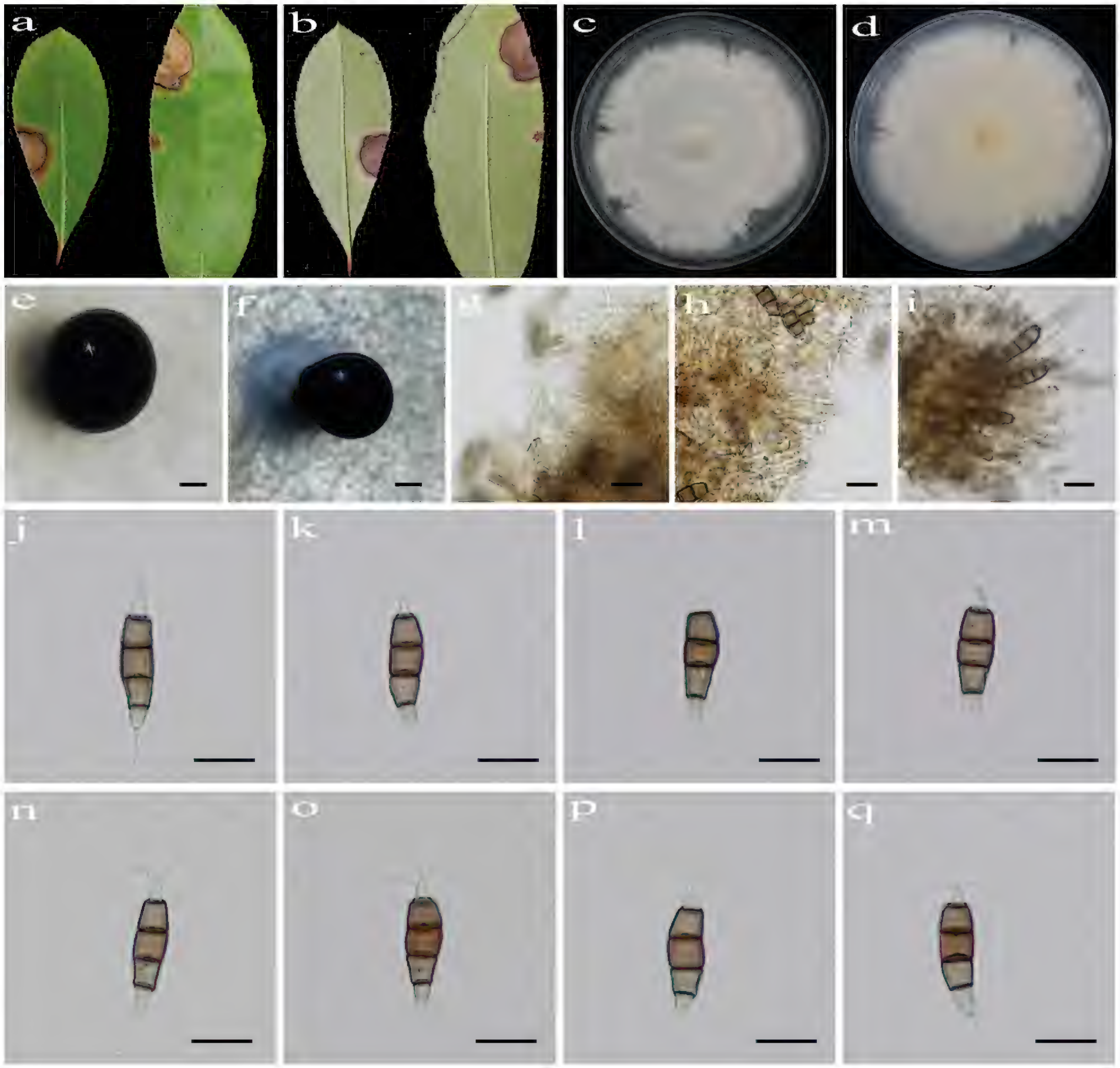

Figure 4. *Pestalotiopsis fraseri* (HJAUP C1693.1, ex-type). **a, b.** Leaf of host plant (front and reverse); **c, d.** Culture on PDA (front and reverse); **e, f.** Conidiomata; **g–i.** Conidiogenous cells and conidia; **j–q.** Conidia. Scale bars: 200 μm (**e, f**); 10 μm (**g–q**).

es, arising from the apex of the apical cell each at a different point, unbranched, 12.3–20.8 μm ($\bar{x}$ = 16.3 μm) long. **Sexual morph:** not observed.

Culture characteristics. Colonies on PDA grow fast, filamentous, reaching 85–90 mm diam. after 5–7 days at 25 °C in light and dark conditions (8 h/16 h), white, with flocculent mycelium and entire edge, forming black conidiomata, and reverse white.

Note. Phylogenetic analyses revealed that the four strains (HJAUP C1693.1^{T}, HJAUP C1693.2, HJAUP C1693.3, and HJAUP C1693.4) of *P. fraseri* form a distinct clade sister to *P. koelreuteriæ* (HJAUP C2757.1^{T} and HJAUP C2757.2) with 100% ML/1.00 BI bootstrap support (Fig. 1). Based on a BLASTn search of *P. fraseri* (HJAUP C1693.1^{T}) and *P. koelreuteriæ* (HJAUP C2757.1^{T}) in GenBank, comparisons of nucleotides showed 13 bp (619/632, including three gaps), 1 bp (296/297, no gaps), and 3 bp (479/482, including one gap) nucleotide differences in the ITS, *tef*1-α, and *tub*2 regions, respectively. Based on a BLASTn search of *P. fraseri*

(HJAUP C1693.1^{T}) and *P. trachycarpicola* (OP068^{T}) in GenBank, comparisons of nucleotides showed 10 bp (530/540, including one gap) and 1 bp (294/295, no gaps) in the ITS and *tef*1-α regions, respectively. Moreover, *P. fraseri* differs from *P. koelreuteriæ* (this study) in its conidia with longer basal appendages (4.6–10.5 µm vs. 3.4–6.7 µm) and longer apical appendages (12.3–20.8 µm vs. 8.1–18.5 µm), and from *P. trachycarpicola* Yan M. Zhang & K.D. Hyde (Zhang et al. 2012b) in its longer basal appendages (4.6–10.5 µm vs. 2.7–5.5 µm). Furthermore, *P. fraseri* can be distinguished from *P. koelreuteriæ* and *P. trachycarpicola* by its different host (*Photinia* × *fraseri* vs. *Koelreuteria paniculata* vs. *Trachycarpus fortunei*).

Pestalotiopsis goeppertiae **M.G. Liao & Jian Ma, sp. nov.**

MycoBank No: 861556

Fig. 5

Type. CHINA • Fujian Province, Fuzhou City, Fuzhou Botanical Garden, on diseased leaves of *Goeppertia makoyana*, 24 October 2023, X.X. Luo (HJAUP M1919, ***holotype***), ex-type living culture HJAUP C1919.1 = HJAUP C1919.2 = HJAUP C1919.3 = HJAUP C1919.4.

Etymology. Named after the genus, *Goeppertia*, from which the fungus was isolated.

Description. Regular leaf spots, grey white in center with brown at margin. Asexual morph on PDA: Conidiomata acervular, globose to clavate, 550–1520 µm diam., superficial, solitary or aggregated in clusters, dark brown. Conidiophores indistinct and reduced to conidiogenous cells. Conidiogenous cells hyaline, smooth, cylindrical to ampulliform. Conidia fusiform, straight or slightly curved, 17.0–23.6 × 5.0–5.9 µm ($\overline{x}$ = 19.5 × 5.5 µm, n = 50), 4-septate, slightly constricted at the septa; basal cell conical, 2.8–4.5 µm ($\overline{x}$ = 3.5 µm), hyaline or sometimes pale brown, smooth, thin-walled, with a single filiform appendage, unbranched, 2.3–6.0 µm ($\overline{x}$ = 3.5 µm) long; three median cells doliiform to cylindrical, smooth, thick-walled, 11.0–14.5 µm ($\overline{x}$ = 12.4 µm), concolorous, pale brown to brown, somewhat constricted at the septa, second cell from the base 3.4–5.1 µm ($\overline{x}$ = 4.2 µm) long, third cell 3.7–4.6 µm ($\overline{x}$ = 4.2 µm) long, fourth cell 3.7–4.9 µm ($\overline{x}$ = 4.2 µm) long); apical cell conical to acute, hyaline, smooth, thin-walled, 3.2–4.1 µm ($\overline{x}$ = 3.7 µm) long, with 2–3 filiform appendages, arising from the apex of the apical cell each at a different point, unbranched, 12.6–21.3 µm ($\overline{x}$ = 15.4 µm) long. **Sexual morph:** not observed.

Culture characteristics. Colonies on PDA grow fast, filamentous, reaching 85–90 mm diam. after 5–7 days at 25 °C in light and dark conditions (8 h/16 h), white, with flocculent mycelium and entire edge, forming black, brown conidiomata, and reverse pale orange.

Note. Phylogenetic analyses revealed that the four strains (HJAUP C1919.1^{T}, HJAUP C1919.2, HJAUP C1919.3, and HJAUP C1919.4) of *P. goeppertiæ* form a distinct clade sister to *P. neolitseæ* (NTUCC 17–011^{T} and CFCC 54590) with 97% ML/0.96 BI bootstrap support (Fig. 1). Based on a BLASTn search of *P. goeppertiæ* (HJAUP C1919.1^{T}) and *P. neolitseæ* (NTUCC 17–011^{T}) in GenBank, comparisons of nucleotides showed 9 bp (248/257, including four gaps) and 1 bp (399/400, no gaps) nucleotide differences in the *tef*1-α and *tub*2 regions, respectively. Moreover, *P. goeppertiæ* differs from *P. neolitseæ* H.A. Ariy. & K.D. Hyde (Ariyawansa and Hyde 2018) in its conidia with a shorter

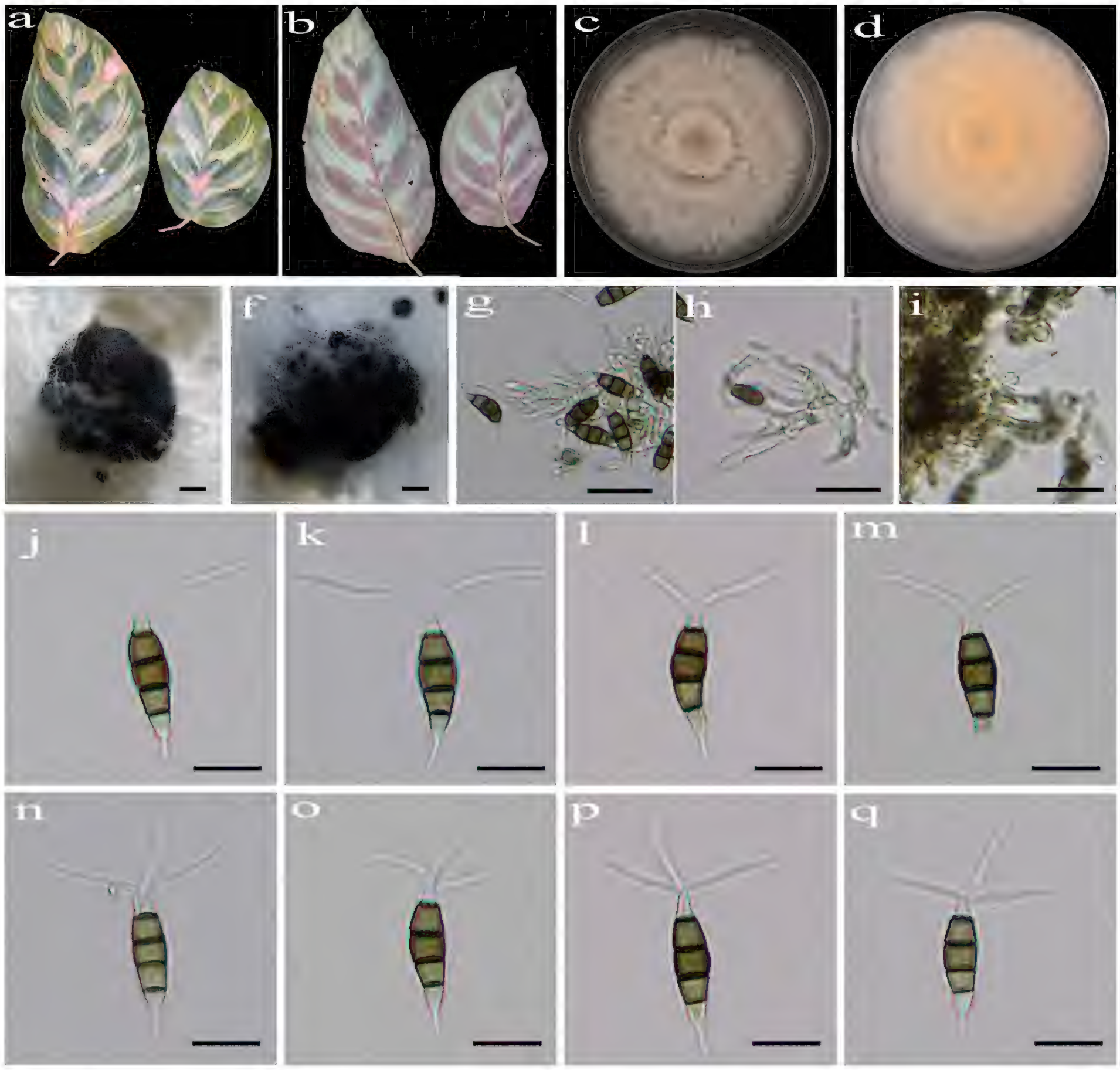

Figure 5. *Pestalotiopsis goeppertiæ* (HJAUP C1919.1, ex-type). **a, b.** Leaf of host plant (front and reverse); **c, d.** Culture on PDA (front and reverse); **e, f.** Conidiomata; **g–i.** Conidiogenous cells and conidia; **j–q.** Conidia. Scale bars: 200 μm (**e, f**); 20 μm (**g–i**); 10 μm (**j–q**).

fourth cell (3.7–4.9 μm vs. 4–5(–6) μm) from the base and longer apical appendages (12.6–21.3 μm vs. (7–)10–15(–17) μm). Furthermore, *P. goeppertiæ* can be distinguished from *P. neolitseæ* by its different host (*Goeppertia makoyana* vs. *Neolitsea villosa*).

***Pestalotiopsis koelreuteriae* M.G. Liao & Jian Ma, sp. nov.**

MycoBank No: 861557

Fig. 6

Type. CHINA • Hunan Province, Zhangjiajie City, Zhangjiajie National Forest Park, on diseased leaves of *Koelreuteria paniculata*, 18 October 2024, M.G. Liao (HJAUP M2757, ***holotype***), ex-type living culture HJAUP C2757.1 = HJAUP C2757.2.

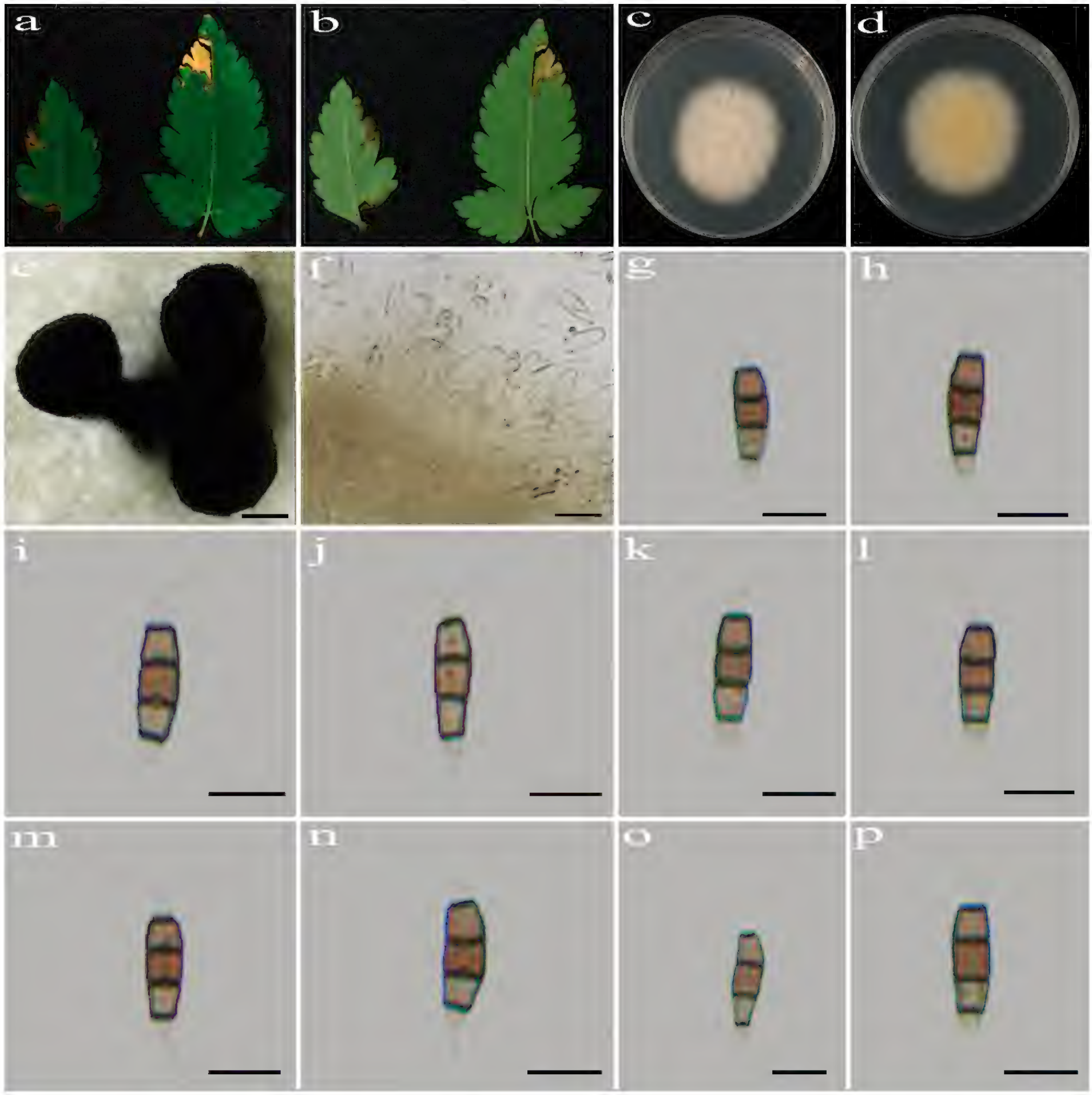

Figure 6. *Pestalotiopsis koelreuteriæ* (HJAUP C2757.1, ex-type). **a, b.** Leaf of host plant (front and reverse); **c, d.** Culture on PDA (front and reverse); **e.** Conidiomata; **f.** Conidiogenous cells and conidia; **g–p.** Conidia. Scale bars: 200 μm (**e**); 10 μm (**f–p**).

Etymology. Named after the genus, *Koelreuteria*, from which the fungus was isolated.

Description. Irregular leaf spots, pale brown in center with brown at margin. Asexual morph on PDA: Conidiomata acervular, globose to clavate, 610–750 μm diam., solitary or aggregated in clusters, black. Conidiophores indistinct and reduced to conidiogenous cells. Conidiogenous cells hyaline, smooth, cylindrical to ampulliform. Conidia fusiform, straight or slightly curved, 18.3–26.9 × 4.1–6.0 μm ($\overline{x}$ = 22.7 × 5.3 μm, n = 50), 4-septate, slightly constricted at the septa; basal cell conical, 2.7–4.6 μm ($\overline{x}$ = 3.9 μm), hyaline or sometimes pale brown, smooth, thin-walled, with a single filiform appendage, unbranched, 3.4–6.7 μm ($\overline{x}$ = 4.9 μm) long; three median cells doliiform to cylindrical, smooth, thick-walled, 12.8–17.3

μm ($\overline{x}$ = 15.2 μm), concolorous, brown, somewhat constricted at the septa, second cell from the base 3.4–6.6 μm ($\overline{x}$ = 4.8 μm) long, third cell 3.4–6.5 μm ($\overline{x}$ = 5.3 μm) long, fourth cell 3.8–6.6 μm ($\overline{x}$ = 5.2 μm) long); apical cell conical to acute, hyaline, smooth, thin-walled, 2.5–5.1 μm ($\overline{x}$ = 3.5 μm) long, with 1–3 (mostly 2) filiform appendages, arising from the apex of the apical cell each at a different point, unbranched, 8.1–18.5 μm ($\overline{x}$ = 13.2 μm) long. **Sexual morph:** not observed.

Culture characteristics. Colonies on PDA grow fast, filamentous, reaching 50–60 mm diam. after 5–7 days at 25 °C in light and dark conditions (8 h/16 h), white, with flocculent mycelium and entire edge, forming black conidiomata, and reverse pale orange.

Note. Phylogenetic analyses revealed that the two strains (HJAUP C2757.1^{T} and HJAUP C2757.2) of *P. koelreuteriæ* form a distinct clade sister to *P. fraseri* (HJAUP C1693.1^{T}, HJAUP C1693.2, HJAUP C1693.3, and HJAUP C1693.4) with 100% ML/1.00 BI bootstrap support (Fig. 1). The nucleotide divergences and morphological differentiations between *P. koelreuteriæ* and *P. fraseri* have been delineated in the preceding section. Comparisons of nucleotides showed 13 bp (2.1%, including three gaps) in the ITS region. Based on the criteria established by Jeewon and Hyde (2016), a divergence of more than 1.5% in the ITS nucleotide sequence can support the recognition of a novel species. Thus, *P. koelreuteriæ* was proposed as a new species.

***Pestalotiopsis machiliana* X.X. Luo & Jian Ma, Mycokeys 109: 229 (2024)**

Index Fungorum: IF902325

Fig. 7

Type. CHINA • Hubei Province, Wuhan City, Wuhan Botanical Garden, on diseased leaves of *Bambusa multiplex* (Lour.) Raeusch. ex Schult. cv. Fernleaf R. A. Young, 24 October 2024, M.G. Liao (HJAUP M2801, living culture HJAUP C2801.1 = HJAUP C2801.2).

Description. Leaf tip lesions, paler brown spots with brown margin between diseased and healthy tissue. **Asexual morph on PDA:** Conidiomata acervular, globose to clavate, 1000–1350 μm diam., solitary or aggregated in clusters, black. Conidiophores indistinct and reduced to conidiogenous cells. Conidiogenous cells hyaline, smooth, cylindrical to ampulliform. Conidia fusiform, straight or slightly curved, 18.1–25.1 × 4.9–6.8 μm ($\overline{x}$ = 21.3 × 5.8 μm, n = 50), 4-septate, slightly constricted at the septa; basal cell conical, 2.9–5.3 μm ($\overline{x}$ = 3.9 μm), hyaline or sometimes pale brown, smooth, thin-walled, with a single filiform appendage, unbranched, 4.4–7.1 μm ($\overline{x}$ = 5.9 μm) long; three median cells doliiform to cylindrical, smooth, thick-walled, 11.2–17.3 μm ($\overline{x}$ = 13.9 μm), concolorous, brown, somewhat constricted at the septa, second cell from the base 3.5–5.7 μm ($\overline{x}$ = 4.6 μm) long, third cell 3.9–5.9 μm ($\overline{x}$ = 4.7 μm) long, fourth cell 3.8–5.7 μm ($\overline{x}$ = 4.6 μm) long); apical cell conical to acute, hyaline, smooth, thin-walled, 2.3–4.8 μm ($\overline{x}$ = 3.5 μm) long, with 2–3 filiform appendages, arising from the apex of the apical cell each at a different point, unbranched, 9.3–20.8 μm ($\overline{x}$ = 14.9 μm) long. **Sexual morph:** not observed.

Culture characteristics. Colonies on PDA grow fast, filamentous, reaching 55–70 mm diam. after 5–7 days at 25 °C in light and dark conditions (8 h /16 h), white, with flocculent mycelium and entire edge, forming black conidiomata, and reverse pale orange.

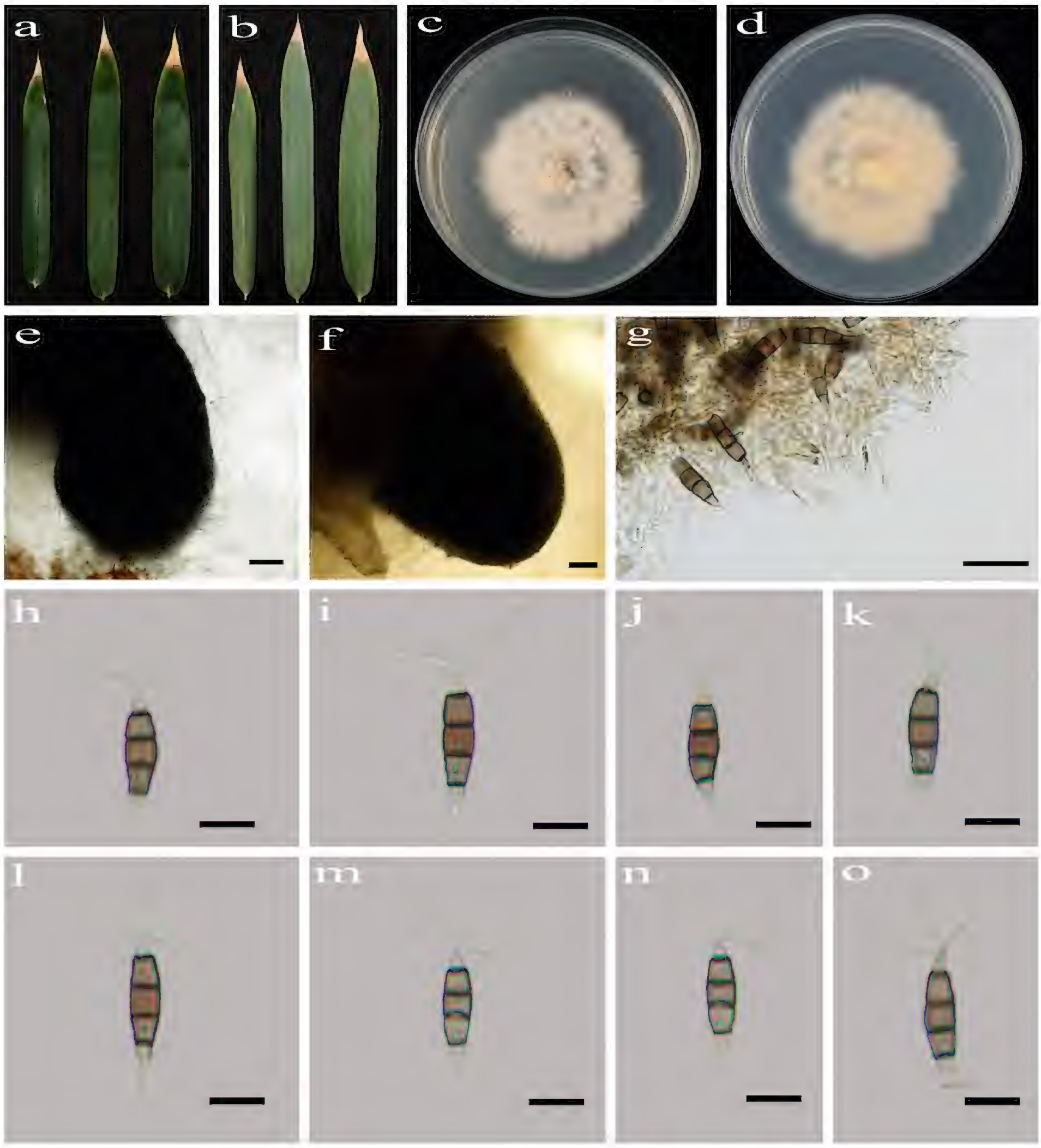

Figure 7. *Pestalotiopsis machiliana* (HJAUP C2801.1). **a, b.** Leaf of host plant (front and reverse); **c, d.** Culture on PDA (front and reverse); **e–f.** Conidiomata; **g.** Conidiogenous cells and conidia; **h–o.** Conidia. Scale bars: 200 μm (**e, f**); 10 μm (**g–o**).

Notes. *Pestalotiopsis machiliana* was introduced by Luo et al. (2024) and isolated from diseased leaves of *Machilus pauhoi* in Jiangxi Province, China. Phylogenetic analyses showed that our new isolates (HJAUP C2801.1 and HJAUP C2801.2) cluster with the group of *P. machiliana* (HJAUP C1704.221, HJAUP C1704.222, HJAUP C1704.223, HJAUP C1790.221^{T}, and HJAUP C1790.222) with 99% ML/1.00 BI bootstrap support (Fig. 1). A BLASTn search of GenBank revealed that the sequences of our new isolate (HJAUP C2801.1) and *P. machiliana* (HJAUP C1790.221^{T}) share 99% similarity (630/632, including

one gap) in ITS, 100% similarity (272/272, no gaps) in *tef*1-α, and 99% similarity (481/482, including one gap) in *tub*2. Morphologically, our isolate aligns well with the original description of *P. machiliana* (Luo et al. 2024). Thus, based on the high morphological similarity and only minor molecular differences, we identified our new isolate as *P. machiliana*.

Discussion

Morphological characteristics have consistently served as a fundamental criterion for the identification of *Pestalotiopsis* species. However, with the continuous increase in the number of *Pestalotiopsis* species, the criteria used for species identification have become increasingly ambiguous (Huanaluek et al. 2021). Maharachchikumbura et al. (2014) previously suggested that continued reliance on conidial size for species delineation within *Pestalotiopsis* is methodologically unsound. In this study, no significant differences were observed in conidial size between *P. acericola* and *P. chiangmaiensis* Y.R. Sun & Yong Wang bis (16.1–24.5 × 5.2–6.9 μm vs. 16–26 × 4–7 μm; Sun et al. 2023), but the two species were clustered into different branches, and the nucleotide differences between *P. acericola* (HJAUP C1856.1^{T}) and *P. chiangmaiensis* (MFLUCC 22–0127^{T}) showed 0.8% (560/565, one gap) in ITS, 7.4% (250/270, eight gaps) in *tef*1-α, and 3.5% (440/456, one gap) in *tub*2. Sun et al. (2023) proposed that the individual cell length characteristics of the three median cells should not be considered criteria for interspecific differentiation, as individual cell length measurements duplicate the description of the total length of the three median cells. Therefore, it was suggested that individual cell length measurements be removed from morphological descriptions to achieve simplification. Additionally, based on phylogenetic analyses, *P. exudata* P. Razaghi, F. Liu & L. Cai and *P. multiappendiculata* P. Razaghi, F. Liu & L. Cai were proposed as novel species (Razaghi et al. 2024), but their conidial septation (4–5-septate) is inconsistent with the generally accepted morphological concept of 5-celled conidia for *Pestalotiopsis* species. Although phylogenetic analyses together with morphology currently serve as an effective approach for identifying *Pestalotiopsis* species, ambiguous morphological concepts can render the classification of these taxa questionable.

To date, 457 species of *Pestalotiopsis* have been recorded in Index Fungorum (Index Fungorum 2025), but molecular data are available in GenBank for only 159 species. The absence of molecular data precludes the resolution of interspecific relationships through phylogenetic analyses and results in substantial ambiguity in the taxonomic placement of morphologically congruent species within the genus. Maharachchikumbura et al. (2012) tested 10 gene regions (*ACT*, *tub2*, *CAL*, *GPDH*, *GS*, ITS, LSU, *RPB1*, SSU, and *tef*1-α) to resolve cryptic *Pestalotiopsis* species and ultimately selected ITS, *tef*1-α, and *tub*2 as the most effective molecular markers. However, recent phylogenetic analyses based on these three markers revealed that some species, such as *P. verruculosa* (MFLUCC 12–0274), lacking *tub*2, and *P. chinensis* (MFLUCC 12–0273), *P. sequoiæ* (MFLUCC 13–0399), and *P. yunnanensis* (HMAS 96359), lacking *tub*2 and *tef*1-α, showed low support values (Hsu et al. 2024; Li et al. 2024; Yin et al. 2024). The low support values for these taxa may be attributed to the ab-

sence of *tef*1-α and/or *tub*2 sequence data, which likely resulted in insufficient phylogenetic information. Thus, completing the ITS, *tef*1-α, and *tub*2 sequence information for *Pestalotiopsis* species is crucial for enabling a more robust discussion of their taxonomic status through phylogenetic analyses. Considering this issue, we conducted phylogenetic analyses using ITS, *tef*1-α, and *tub*2 sequences, and our newly obtained 21 strains nested within the genus *Pestalotiopsis* formed six independent lineages with reliable support values and can be proposed as five new phylogenetic species, namely *P. acericola*, *P. corchorifolii*, *P. fraseri*, *P. goeppertiæ*, and *P. koelreuteriæ*, and one known species, *P. machiliana*.

Appendages are often used as an important basis for the morphological identification of *Pestalotiopsis* species, but studies have confirmed their critical roles in conidial dispersal and host colonization (Nag Raj 1993; Gareth Jones 2006; Crous et al. 2012). This facilitates the widespread colonization of various plants by *Pestalotiopsis* as endophytes and pathogens, thereby enhancing host diversity and competitiveness for ecological niches. *Pestalotiopsis* causes diseases on a variety of host plants as a pathogen, including tea, ericaceous plants, grapes, pomegranates, blueberries, and other crops, resulting in significant economic losses (Horikawa 1986; Xu et al. 1999; McQuilken and Hopkins 2004; Keith et al. 2006; Espinoza et al. 2008; Joshi et al. 2009). Many *Pestalotiopsis* species, when living as endophytes, have been demonstrated to produce numerous secondary metabolites with diverse structural characteristics (Xu et al. 2010), and previous studies have reported over 160 different compounds isolated from *Pestalotiopsis* species, which demonstrate significant potential in antifungal and antimicrobial activities and compound synthesis (Xu et al. 2014). Thus, further research is necessary to contribute to the fields of plant pathology and fungal taxonomy and to explore their functional roles.

Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Use of AI

No use of AI was reported.

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Author contributions

Sampling: X.X.L. and M.G.L.; fungal isolation: X.X.L. and M.G.L.; microscopy: X.X.L., M.G.L., and Z.H.X.; description and phylogenetic analyses: M.G.L., F.H.G., and L.H.Z.; writing – original draft preparation: M.G.L.; writing – review and editing: R.Q.C., X.G.Z., and J.M. All authors read and approved the final manuscript.

Author ORCIDs

Ming-Gen Liao https://orcid.org/0009-0001-9537-1773
Zhao-Huan Xu https://orcid.org/0009-0008-2641-7783
Xiu-Guo Zhang https://orcid.org/0000-0001-9733-8494
Jian Ma https://orcid.org/0000-0001-9783-1860

Data availability

All of the data that support the findings of this study are available in the main text or Supplementary Information.

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Supplementary material 1

Supplementary file S1, file S2 and file S3

Authors: Ming-Gen Liao, Fang-Hua Guo, Xing-Xing Luo, Lian-Hu Zhang, Ru-Qiang Cui, Zhao-Huan Xu, Xiu-Guo Zhang, Jian Ma

Data type: zip

Explanation note: **file S1.** The concatenated ITS, tef1-α and tub2 sequences; **file S2.** The sequence alignment based on ITS, tef1-α and tub2 regions, respectively; **file S3.** The PTP analysis for the Pestalotiopsis species complex and related taxa.

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